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## SEQUENCE LISTING

<110> Khodadoust, Mehran M.  
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<120> NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND  
STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES  
THEREFOR

<130> MNI-121CP

<140>  
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<150> PCT/US00/02125  
<151> 2000-01-27

<150> 09/448,076  
<151> 1999-11-23

<150> 09/276,400  
<151> 1999-03-25

<150> 60/117,580  
<151> 1999-01-27

<150> 09/014,195  
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<151> 1998-05-29

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<150> 09/049,799  
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<160> 176

<170> PatentIn Ver. 2.0

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<212> DNA

<213> Homo sapiens

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CDS

<222> (43)..(573)

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tgt gtt tcc ctt tgg ctc ctg ggt aca ata ctg ata ttg tgc tca gta      102
Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile Leu Cys Ser Val
      5           10                  15                  20

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gac aac cac ggt ctc agg aga tgt ctg att tcc aca gac atg cac cat 150  
 Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr Asp Met His His  
 25 30 35

ata gaa gag agt ttc caa gaa atc aaa aga gcc atc caa gct aag gac 198  
Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile Gln Ala Lys Asp  
40 45 50

acc ttc cca aat gtc act atc ctg tcc aca ttg gag act ctg cag atc 246  
 Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu Thr Leu Gln Ile  
           55              60              65

att aag ccc tta gat gtg tgc tgc gtg acc aag aac ctc ctg gcg ttc 294  
Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn Leu Leu Ala Phe  
70 75 80

tac gtg gac agg gtg ttc aag gat cat cag gag cca aac ccc aaa atc 342  
 Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro Asn Pro Lys Ile  
 85 90 95 100

ttg aga aaa atc agc agc att gcc aac tct ttc ctc tac atg cag aaa 390  
 Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys  
 105 110 115

act ctg cgg caa tgt cag gaa cag agg cag tgt cac tgc agg cag gaa 438  
 Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu  
                  120                 125                 130

gcc acc aat gcc acc aga gtc atc cat gac aac tat gat cag ctg gag 486  
 Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu  
                  135                 140                 145

gtc cac gct gct gcc att aaa tcc ctg gga gag ctc gac gtc ttt cta 534  
 Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu  
 150 155 160

gcc tgg att aat aag aat cat gaa gta atg tcc tca gct tgatgacaag	583
Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser Ala	
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gaacctgtat agtgatccag gcatgcacac cccctgtgcg gtttactgtg ggagacagcc	643
caccttgaag ggaaaggaga tggggaggc cccttcgcgc tgaaagtccc actggctggc	703
ctcaggctgt ctatttcgc tcgaaaatag ccaaaaagtc tactgtggta tttgtataa	763
actctatctg ctgaaaggc ctgcaggcca tcctggagt aaaggctgc cttccatct	823
aatttattgt gaagtcatat agtccatgtc tgtgtatgtga gccaaatgtat atcctgttagt	883
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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr	
20	25
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Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile	
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Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu	
50	55
	60

Thr Leu Gin Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn	
65	70
	75
	80

Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro	
85	90
	95

Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu	
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Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His	
115	120
	125

Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr	
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Asp Gln Leu Glu Val His Ala Ala Ile Lys Ser Leu Gly Glu Leu	
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Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser	
165	170
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Ala

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(531)

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ttg tgc tca gta gac aac cac ggt ctc agg aga tgt ctg att tcc aca	96
Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr	
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gac atg cac cat ata gaa gag agt ttc caa gaa atc aaa aga gcc atc	144
Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile	
35 40 45	

caa gct aag gac acc ttc cca aat gtc act atc ctg tcc aca ttg gag	192
Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu	
50 55 60	

act ctg cag atc att aag ccc tta gat gtg tgc tgc gtg acc aag aac	240
Thr Leu Gln Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn	
65 70 75 80	

ctc ctg qcq ttc tac gtg gac agg gtg ttc aag gat cat cag gag cca	288
Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro	
85 90 95	

aac ccc aaa atc ttg aga aaa atc agc agc att gcc aac tct ttc ctc	336
Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu	
100 105 110	

tac atg cag aaa act ctg cgg caa tgt cag gaa cag agg cag tgt cac	384
Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His	
115 120 125	

tgc agg cag gaa gcc acc aat gcc acc aga gtc atc cat gac aac tat	432
Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr	
130 135 140	

gat cag ctg gag gtc cac gct gct gcc att aaa tcc ctg gga gag ctc	480
Asp Gln Leu Glu Val His Ala Ala Ile Lys Ser Leu Gly Glu Leu	
145 150 155 160	

gac gtc ttt cta gcc tgg att aat aag aat cat gaa gta atg tcc tca	528
Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser	
165 170 175	

gct	531
Ala	

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Val Thr Ile Leu Ser Thr Leu Glu Thr Leu Gln Ile Ile Lys Pro Leu  
35 40 45  
  
Asp Val Cys Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg  
50 55 60  
  
Val Phe Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile  
65 70 75 80  
  
Ser Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln  
85 90 95  
  
Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn Ala  
100 105 110  
  
Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His Ala Ala  
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Lys Asn His Glu Val Met Ser Ser Ala  
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Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe  
35 40 45  
  
Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu  
50 55 60  
  
Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys  
65 70 75 80

- 6 -

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro  
 85 90 95

Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu  
 100 105 110

Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg  
 115 120 125

Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn  
 130 135 140

Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu  
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Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile  
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Arg Asn

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Phe Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe  
 35 40 45

Ser Gln Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile  
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Leu Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys  
 65 70 75 80

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro  
 85 90 95

Gln Ala Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu  
 100 105 110

Gly Glu Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg  
 115 120 125

Phe Leu Lys Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser  
 130 135 140

Asp Phe Asn Lys Leu Glu Asp Gln Gly Val Tyr Lys Ala Met Asn Glu  
 145 150 155 160

Phe Asp Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met  
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Lys Ser

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<212> PRT  
<213> *Homo sapiens*

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Leu Pro Thr Ser Leu Pro His Met Leu His Glu Leu Arg Ala Ala Phe  
35 40 45

Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Met  
50 55 60

Leu Leu Asp Gly Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys  
65 70 75 80

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro  
85 90 95

Gln Ala Glu Asn His Ser Thr Asp Gln Glu Lys Asp Lys Val Asn Ser  
           100                 105                 110

Leu Gly Glu Lys Leu Lys Thr Leu Arg Val Arg Leu Arg Arg Cys His  
115 120 125

Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys  
130 135 140

Ser Ala Phe Ser Lys Leu Gln Glu Lys Gly Val Tyr Lys Ala Met Ser  
145 150 155 160

Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Thr Lys  
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Met Lys Asn

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                  20                     25                     30

Ser Cys Gln Val Thr Gly Val Val Leu Pro Glu Leu Trp Glu Ala Phe  
                  35                     40                     45

Trp Thr Val Lys Asn Thr Val Gln Thr Gln Asp Asp Ile Thr Ser Ile  
                  50                     55                     60

Arg Leu Leu Lys Pro Gln Val Leu Arg Asn Val Ser Gly Ala Glu Ser  
                  65                     70                     75                     80

Cys Tyr Leu Ala His Ser Leu Leu Lys Phe Tyr Leu Asn Thr Val Phe  
                  85                     90                     95

Lys Asn Tyr His Ser Lys Ile Ala Lys Phe Lys Val Leu Arg Ser Phe  
                  100                    105                     110

Ser Thr Leu Ala Asn Asn Phe Ile Val Ile Met Ser Gln Leu Gln Pro  
                  115                    120                     125

Ser Lys Asp Asn Ser Met Leu Pro Ile Ser Glu Ser Ala His Gln Arg  
                  130                    135                     140

Phe Leu Leu Phe Arg Arg Thr Phe Lys Gln Leu Asp Thr Glu Val Ala  
                  145                    150                     155                     160

Leu Val Lys Ala Phe Gly Glu Val Asp Ile Leu Leu Thr Trp Met Gln  
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Lys Phe Tyr His Leu  
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<212> PRT

<213> Homo sapiens

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                  20                    25                     30

Gln Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala  
                  35                    40                     45

Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg Leu  
                  50                    55                     60

Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser Cys Tyr  
                  65                    70                     75                     80

Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val Phe Lys Asn  
                  85                    90                     95

Tyr His Asn Arg Thr Val Glu Val Arg Thr Leu Lys Ser Phe Ser Thr  
                  100                    105                     110

Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln Leu Gln Pro Ser Gln  
 115 120 125

Glu Asn Glu Met Phe Ser Ile Arg Asp Ser Ala His Arg Arg Phe Leu  
 130 135 140

Leu Phe Arg Arg Ala Phe Lys Gln Leu Asp Val Glu Ala Ala Leu Thr  
 145 150 155 160

Lys Ala Leu Gly Glu Val Asp Ile Leu Leu Thr Trp Met Gln Lys Phe  
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Tyr Lys Leu

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ctcgcccaag gccttccctg cc atg cga cct gtc agt gtc tgg cag tgg agc 172  
 Met Arg Pro Val Ser Val Trp Gln Trp Ser  
 1 5 10

ccc tgg ggg ctg ctg ctg tgc ctg tgc agt tcg tgc ttg ggg tct 220  
 Pro Trp Gly Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser  
 15 20 25

ccg tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt 268  
 Pro Ser Pro Ser Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu  
 30 35 40

ccg ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg 316  
 Arg Phe Arg Leu Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val  
 45 50 55

gag ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc 364  
 Glu Ile Gln Arg Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe  
 60 65 70

acg ctg cag gct gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag 412  
 Thr Leu Gln Ala Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu  
 75 80 85 90

gcc aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc 460  
 Ala Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg  
 95 100 105

atc tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act Ile Trp Leu Asp Asn Leu Ser Cys Ser Gly Thr Glu Gln Ser Val Thr 110 115 120	508
gaa tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag Glu Cys Ala Ser Arg Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu 125 130 135	556
gat gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tcg gac Asp Ala Gly Val Ile Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp 140 145 150	604
tcc aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga Ser Asn Val Ile Glu Val His His Leu Gln Val Glu Glu Val Arg 155 160 165 170	652
att cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag Ile Arg Pro Ala Val Gly Trp Gly Arg Arg Pro Leu Pro Val Thr Glu 175 180 185	700
ggg ctg gtg gaa gtc agg ctt cct gac ggc tgg tcg caa gtg tgc gac Gly Leu Val Glu Val Arg Leu Pro Asp Gly Trp Ser Gln Val Cys Asp 190 195 200	748
aaa ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc Lys Gly Trp Ser Ala His Asn Ser His Val Val Cys Gly Met Leu Gly 205 210 215	796
ttc ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc Phe Pro Ser Glu Lys Arg Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala 220 225 230	844
caa cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc Gln Arg Gln Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly 235 240 245 250	892
acg gag gcc cac ctc tcc ctc tgt tcc ctg gag ttc tat cgt gcc aat Thr Glu Ala His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn 255 260 265	940
gac acc gcc agg tgc cct ggg ggg ggc cct gca gtg gtg agc tgt gtg Asp Thr Ala Arg Cys Pro Gly Gly Pro Ala Val Val Ser Cys Val 270 275 280	988
cca ggc cct gtc tac gca tcc agt ggc cag aag aag caa caa cag Pro Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln 285 290 295	1036
tcg aag cct cag ggg gag gcc cgt gtc cgt cta aag ggc ggc gcc cac Ser Lys Pro Gln Gly Glu Ala Arg Val Arg Leu Lys Gly Gly Ala His 300 305 310	1084
cct gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca Pro Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr 315 320 325 330	1132
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gag ctg ggc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg Glu Leu Gly Phe Gly Ser Ala Arg Glu Ala Leu Ser Gly Ala Arg Met 350	355	360	1228	
ggg cag ggc atg ggt gct atc cac ctg agt gaa gtt cgc tgc tct gga Gly Gln Gly Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly 365	370	375	1276	
cag gag ctc tcc ctc tgg aag tgc ccc cac aag aac atc aca gct gag Gln Glu Leu Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala Glu 380	385	390	1324	
gat tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac Asp Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr 395	400	405	410	1372
act ggg gca gag acc agg atc cga ctc agt ggg ggc cgc agc caa cat Thr Gly Ala Glu Thr Arg Ile Arg Leu Ser Gly Gly Arg Ser Gln His 415	420	425	1420	
gag ggg cga gtc gag gtgcaa ata ggg gga cct ggg ccc ctt cgc tgg Glu Gly Arg Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp 430	435	440	1468	
ggc ctc atc tgt ggg gat gac tgg ggg acc ctg gag gcc atg gtg gcc Gly Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met Val Ala 445	450	455	1516	
tgt agg caa ctg ggt ctg ggc tac gcc aac cac ggc ctg cag gag acc Cys Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln Glu Thr 460	465	470	1564	
tgg tac tgg gac tct ggg aat ata aca gag gtg gtg atg agt gga gtg Trp Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser Gly Val 475	480	485	490	1612
cgc tgc aca ggg act gag ctg tcc ctg gat cag tgt gcc cat cat ggc Arg Cys Thr Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His His Gly 495	500	505	1660	
acc cac atc acc tgc aag agg aca ggg acc cgc ttc act gct gga gtc Thr His Ile Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala Gly Val 510	515	520	1708	
atc tgt tct gag act gca tca gat ctg ttg ctg cac tca gca ctg gtg Ile Cys Ser Glu Thr Ala Ser Asp Leu Leu His Ser Ala Leu Val 525	530	535	1756	
cag gag acc gcc tac atc gaa gac cgg ccc ctg cat atg ttg tac tgt Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr Cys 540	545	550	1804	
gct gcg gaa gag aac tgc ctg gcc agc tca gcc cgc tca gcc aac tgg Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp 555	560	565	570	1852
ccc tat ggt cac cgg cgt ctg ctc cga ttc tcc tcc cag atc cac aac Pro Tyr Gly His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn 575	580	585	1900	

ctg gga cga gct gac ttc agg ccc aag gct ggg cgc cac tcc tgg gtg Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp Val 590 595 600	1948
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tat gat atc ctc acc cca aat ggc acc aag gtg gct gag ggc cac aaa Tyr Asp Ile Leu Thr Pro Asn Gly Thr Lys Val Ala Glu Gly His Lys 620 625 630	2044
gct agt ttc tgt ctc gaa gac act gag tgt cag gag gat gtc tcc aag Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser Lys 635 640 645 650	2092
cgg tat gag tgt gcc aac ttt gga gag caa ggc atc act gtg ggt tgc Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Gly Cys 655 660 665	2140
tgg gat ctc tac cgg cat gac att gac tgt cag tgg att gac atc acg Trp Asp Leu Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr 670 675 680	2188
gat gtg aag cca gga aac tac att ctc cag gtt gtc atc aac cca aac Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro Asn 685 690 695	2236
ttt gaa gta gca gag agt gac ttt acc aac aat gca atg aaa tgt aac Phe Glu Val Ala Glu Ser Asp Phe Thr Asn Asn Ala Met Lys Cys Asn 700 705 710	2284
tgc aaa tat gat gga cat aga atc tgg gtg cac aac tgc cac att ggt Cys Lys Tyr Asp Gly His Arg Ile Trp Val His Asn Cys His Ile Gly 715 720 725 730	2332
gat gcc ttc agt gaa gag gcc aac agg agg ttt gaa cgc tac cct ggc Asp Ala Phe Ser Glu Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly 735 740 745	2380
cag acc agc aac cag att atc taagtgccac tgccctctgc aaaccaccac Gln Thr Ser Asn Gln Ile Ile 750	2431
tggcccctaa tggcagggt ctgaggctgc cattacctca ggagcttacc aagaaaccca	2491
tgtcagcaac cgcaactatc agaccatgca ctatggatgt ggaactgtca agcagaagtt	2551
ttcacccctcc ttcataggcc agctgtcaat atctgttagcc aagcatggaa atcttgctc	2611
ccaggcccaag caccgagcag aacagaccag agcccaccac accacaaga gcagcacctg	2671
actaactgcc cacaaaaagat ggcagcagct cattttcttt aataggaggt caggatggtc	2731
agctccagta tctcccctaa gtttaggggg atacagcttt acctctagcc ttttgtgg	2791
ggaaaaagatc cagccctccc acctcattt ttactataat atgttgctag gtataat	2851
tttttatata aaaagtgttt ctgtgattct tcagaaaaaa aaaaaaaaaa aaaaaaaaaa	2911

aaaaaaaaaa

2920

<210> 11  
<211> 753  
<212> PRT  
<213> Homo sapiens

<400> 11  
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu  
1 5 10 15

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly  
20 25 30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly  
35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly  
50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His  
65 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His  
85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu  
100 105 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly  
115 120 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys  
130 135 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val  
145 150 155 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly  
165 170 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg  
180 185 190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His  
195 200 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg  
210 215 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser  
225 230 235 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser  
245 250 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro  
260 265 270

Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala  
 275 280 285  
 Ala Ser Ser Gly Gln Lys Lys Gln Gln Ser Lys Pro Gln Gly Glu  
 290 295 300  
 Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val  
 305 310 315 320  
 Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp  
 325 330 335  
 Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser  
 340 345 350  
 Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala  
 355 360 365  
 Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp  
 370 375 380  
 Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln  
 385 390 395 400  
 Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg  
 405 410 415  
 Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val  
 420 425 430  
 Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp  
 435 440 445  
 Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu  
 450 455 460  
 Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly  
 465 470 475 480  
 Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu  
 485 490 495  
 Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys  
 500 505 510  
 Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala  
 515 520 525  
 Ser Asp Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile  
 530 535 540  
 Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys  
 545 550 555 560  
 Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg  
 565 570 575  
 Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe  
 580 585 590

- 15 -

Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly  
 595 600 605

His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro  
 610 615 620

Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu  
 625 630 635 640

Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn  
 645 650 655

Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His  
 660 665 670

Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn  
 675 680 685

Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser  
 690 695 700

Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His  
 705 710 715 720

Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu  
 725 730 735

Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile  
 740 745 750

Ile

<210> 12

<211> 2262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2259)

<400> 12

atg cga cct gtc agt gtc tgg cag tgg agc ccc tgg ggg ctg ctg ctg  
 Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu  
 1 5 10 15

tgc ctg ctg tgc agt tcg ttg ggg tct ccg tcc cct tcc acg ggc  
 Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly  
 20 25 30

cct gag aag aag gcc ggg agc cag ggg ctt cgg ttc cgg ctg gct ggc  
 Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly  
 35 40 45

ttc ccc agg aag ccc tac gag ggc cgc gtg gag ata cag cga gct ggt  
 Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly  
 50 55 60

gaa tgg ggc acc atc tgc gat gat gac ttc acg ctg cag gct gcc cac		240
Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His		
65	70	75
80		
atc ctc tgc cgg gag ctg ggc ttc aca gag gcc aca ggc tgg acc cac		288
Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His		
85	90	95
agt gcc aaa tat ggc cct gga aca ggc cgc atc tgg ctg gac aac ttg		336
Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu		
100	105	110
agc tgc agt ggg acc gag cag agt gtg act gaa tgt gcc tcc cgg ggc		384
Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly		
115	120	125
tgg ggg aac agt gac tgt acg cac gat gag gat gct ggg gtc atc tgc		432
Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys		
130	135	140
aaa gac cag cgc ctc cct ggc ttc tcg gac tcc aat gtc att gag gta		480
Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val		
145	150	155
160		
gag cat cac ctgcaa gtg gag gag gtg cga att cga ccc gcc gtt ggg		528
Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly		
165	170	175
tgg ggc aga cga ccc ctg ccc gtg acg gag ggg ctg gtg gaa gtc agg		576
Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg		
180	185	190
ctt cct gac ggc tgg tcg caa gtg tcg gac aaa ggc tgg agc gcc cac		624
Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His		
195	200	205
aac agc cac gtg gtc tgc ggg atg ctg ggc ttc ccc agc gaa aag agg		672
Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg		
210	215	220
gtc aac gcg gcc ttc tac agg ctg cta gcc caa cgg cag caa cac tcc		720
Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser		
225	230	235
240		
ttt ggt ctg cat ggg gtg gcg tgc gtg ggc acg gag gcc cac ctc tcc		768
Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser		
245	250	255
ctc tgt tcc ctg gag ttc tat cgt gcc aat gac acc gcc agg tgc cct		816
Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro		
260	265	270
ggg ggg ggc cct gca gtg gtg acg tgt gtg cca ggc cct gtc tac gcg		864
Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala		
275	280	285
gca tcc agt ggc cag aag caa caa cag tcg aag cct cag ggg gag		912
Ala Ser Ser Gly Gln Lys Lys Gln Gln Ser Lys Pro Gln Gly Glu		
290	295	300

gcc cgt gtc cgt cta aag ggc ggc gcc cac cct gga gag ggc cgg gta Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val 305 310 315 320	960
gaa gtc ctg aag gcc agc aca tgg ggc aca gtc tgt gac cgc aag tgg Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp 325 330 335	1008
gac ctg cat gca gcc agc gtg gtg tgt cgg gag ctg ggc ttc ggg agt Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser 340 345 350	1056
gct cga gaa gct ctg agt ggc gct cgc atg ggg cag ggc atg ggt gct Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala 355 360 365	1104
atc cac ctg agt gaa gtt cgc tgc tct gga cag gag ctc tcc ctc tgg Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp 370 375 380	1152
aag tgc ccc cac aag aac atc aca gct gag gat tgt tca cat agc cag Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln 385 390 395 400	1200
gat gcc ggg gtc cgg tgc aac cta cct tac act ggg gca gag acc agg Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg 405 410 415	1248
atc cga ctc agt ggg ggc cgc agc caa cat gag ggg cga gtc gag gtg Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val 420 425 430	1296
caa ata ggg gga cct ggg ccc ctt cgc tgg ggc ctc atc tgt ggg gat Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp 435 440 445	1344
gac tgg ggg acc ctg gag gcc atg gtg gcc tgt agg caa ctg ggt ctg Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu 450 455 460	1392
ggc tac gcc aac cac ggc ctg cag gag acc tgg tac tgg gac tct ggg Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly 465 470 475 480	1440
aat ata aca gag gtg gtg atg agt gga gtg cgc tgc aca ggg act gag Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu 485 490 495	1488
ctg tcc ctg gat cag tgt gcc cat cat ggc acc cac atc acc tgc aag Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys 500 505 510	1536
agg aca ggg acc cgc ttc act gct gga gtc atc tgt tct gag act gca Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala 515 520 525	1584
tca gat ctg ttg ctg cac tca gca ctg gtg cag gag acc gcc tac atc Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile 530 535 540	1632

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gaa gac cgg ccc ctg cat atg ttg tac tgt gct gcg gaa gag aac tgc Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys 545 550 555 560	1680
ctg gcc agc tca gcc cgc tca gcc aac tgg ccc tat ggt cac cgg cgt Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg 565 570 575	1728
ctg ctc cga ttc tcc tcc cag atc cac aac ctg gga cga gct gac ttc Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe 580 585 590	1776
agg ccc aag gct ggg cgc cac tcc tgg gtg tgg cac gag tgc cat ggg Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly 595 600 605	1824
cat tac cac agc atg gac atc ttc act cac tat gat atc ctc acc cca His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro 610 615 620	1872
aat ggc acc aag gtg gct gag ggc cac aaa gct agt ttc tgt ctc gaa Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu 625 630 635 640	1920
gac act gag tgt cag gag gat gtc tcc aag cgg tat gag tgt gcc aac Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn 645 650 655	1968
ttt gga gag caa ggc atc act gtg ggt tgc tgg gat ctc tac cgg cat Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His 660 665 670	2016
gac att gac tgt cag tgg att gac atc acg gat gtg aag cca gga aac Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn 675 680 685	2064
tac att ctc cag gtt gtc atc aac cca aac ttt gaa gta gca gag agt Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser 690 695 700	2112
gac ttt acc aac aat gca atg aaa tgt aac tgc aaa tat gat gga cat Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His 705 710 715 720	2160
aga atc tgg gtg cac aac tgc cac att ggt gat gcc ttc agt gaa gag Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu 725 730 735	2208
gcc aac agg agg ttt gaa cgc tac cct ggc cag acc agc aac cag att Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile 740 745 750	2256
atc taa Ile	2262

<210> 13  
<211> 38  
<212> PRT  
<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: (SRRD)  
consensus sequence

&lt;220&gt;

&lt;223&gt; Any occurrences of Xaa may be any amino acid

&lt;400&gt; 13

Gly Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15Trp Gly Xaa Xaa Cys Xaa  
20 25 30Xaa Cys Xaa Xaa Xaa Gly  
35

&lt;210&gt; 14

&lt;211&gt; 417

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys  
1 5 10 15Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro  
20 25 30Arg Glu Pro Pro Ala Ala Pro Gly Ala Trp Arg Gln Gln Ile Gln Trp  
35 40 45Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr  
50 55 60Gln Pro Gln Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala  
65 70 75 80Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp  
85 90 95Asn Arg Thr Ala Ala Gly Arg Thr Arg Thr Ala Gly Ser Ser Gly Val  
100 105 110Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly  
115 120 125Tyr Ser Thr Ser Arg Ala Arg Glu Ala Gly Pro Ser Arg Ala Glu Asn  
130 135 140Gln Thr Ala Pro Gly Glu Val Pro Ala Leu Ser Asn Leu Arg Pro Pro  
145 150 155 160Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys  
165 170 175

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Tyr	Ser	Asp	Asp	Asn	Pro	Tyr	Tyr	Asn	Tyr	Tyr	Asp	Thr	Tyr	Glu	Arg
180								185						190	
Pro	Arg	Pro	Gly	Gly	Arg	Tyr	Arg	Pro	Gly	Tyr	Gly	Thr	Gly	Tyr	Phe
195							200						205		
Gln	Tyr	Gly	Leu	Pro	Asp	Leu	Val	Ala	Asp	Pro	Tyr	Tyr	Ile	Gln	Ala
210				215							220				
Ser	Thr	Tyr	Val	Gln	Lys	Met	Ser	Met	Tyr	Asn	Leu	Arg	Cys	Ala	Ala
225				230						235				240	
Glu	Glu	Asn	Cys	Leu	Ala	Ser	Thr	Ala	Tyr	Arg	Ala	Asp	Val	Arg	Asp
245								250					255		
Tyr	Asp	His	Arg	Val	Leu	Leu	Arg	Phe	Pro	Gln	Arg	Val	Lys	Asn	Gln
260							265					270			
Gly	Thr	Ser	Asp	Phe	Leu	Pro	Ser	Arg	Pro	Arg	Tyr	Ser	Trp	Glu	Trp
275					280						285				
His	Ser	Cys	His	Gln	His	Tyr	His	Ser	Met	Asp	Glu	Phe	Ser	His	Tyr
290					295						300				
Asp	Leu	Leu	Asp	Ala	Asn	Thr	Gln	Arg	Arg	Val	Ala	Glu	Gly	His	Lys
305					310					315				320	
Ala	Ser	Phe	Cys	Leu	Glu	Asp	Thr	Ser	Cys	Asp	Tyr	Gly	Tyr	His	Arg
325								330					335		
Arg	Phe	Ala	Cys	Thr	Ala	His	Thr	Gln	Gly	Leu	Ser	Pro	Gly	Cys	Tyr
340							345					350			
Asp	Thr	Tyr	Gly	Ala	Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	Ile	Thr	Asp
355						360						365			
Val	Lys	Pro	Gly	Asn	Tyr	Ile	Leu	Lys	Val	Ser	Val	Asn	Pro	Ser	Tyr
370						375						380			
Leu	Val	Pro	Glu	Ser	Asp	Tyr	Thr	Asn	Asn	Val	Val	Arg	Cys	Asp	Ile
385					390					395				400	
Arg	Tyr	Thr	Gly	His	His	Ala	Tyr	Ala	Ser	Gly	Cys	Thr	Ile	Ser	Pro
405							410						415		

Tyr

<210> 15

<211> 574

<212> PRT

<213> Homo sapiens

<400> 15

Met	Ala	Leu	Ala	Arg	Gly	Ser	Arg	Gln	Leu	Gly	Ala	Leu	Val	Trp	Gly
1				5					10				15		

Ala	Cys	Leu	Cys	Val	Leu	Val	His	Gly	Gln	Gln	Ala	Gln	Pro	Gly	Gln
20							25					30			

Gly Ser Asp Pro Ala Arg Trp Arg Gln Leu Ile Gln Trp Glu Asn Asn  
35 40 45

Gly Gln Val Tyr Ser Leu Leu Asn Ser Gly Ser Glu Tyr Val Pro Ala  
50 55 60

Gly Pro Gln Arg Ser Glu Ser Ser Ser Arg Val Leu Leu Ala Gly Ala  
65 70 75 80

Pro Gln Ala Gln Gln Arg Arg Ser His Gly Ser Pro Arg Arg Arg Gln  
85 90 95

Ala Pro Ser Leu Pro Leu Pro Gly Arg Val Gly Ser Asp Thr Val Arg  
100 105 110

Gly Gln Ala Arg His Pro Phe Gly Phe Gly Gln Val Pro Asp Asn Trp  
115 120 125

Arg Glu Val Ala Val Gly Asp Ser Thr Gly Met Ala Leu Ala Arg Thr  
130 135 140

Ser Val Ser Gln Gln Arg His Gly Gly Ser Ala Ser Ser Val Ser Ala  
145 150 155 160

Ser Ala Phe Ala Ser Thr Tyr Arg Gln Gln Pro Ser Tyr Pro Gln Gln  
165 170 175

Phe Pro Tyr Pro Gln Ala Pro Phe Val Ser Gln Tyr Glu Asn Tyr Asp  
180 185 190

Pro Ala Ser Arg Thr Tyr Asp Gln Gly Phe Val Tyr Tyr Arg Pro Ala  
195 200 205

Gly Gly Gly Val Gly Ala Gly Ala Ala Val Ala Ser Ala Gly Val  
210 215 220

Ile Tyr Pro Tyr Gln Pro Arg Ala Arg Tyr Glu Glu Tyr Gly Gly  
225 230 235 240

Glu Glu Leu Pro Glu Tyr Pro Pro Gln Gly Phe Tyr Pro Ala Pro Glu  
245 250 255

Arg Pro Tyr Val Pro Pro Pro Pro Pro Pro Asp Gly Leu Asp Arg  
260 265 270

Arg Tyr Ser His Ser Leu Tyr Ser Glu Gly Thr Pro Gly Phe Glu Gln  
275 280 285

Ala Tyr Pro Asp Pro Gly Pro Glu Ala Ala Gln Ala His Gly Gly Asp  
290 295 300

Pro Arg Leu Gly Trp Tyr Pro Pro Tyr Ala Asn Pro Pro Pro Glu Ala  
305 310 315 320

Tyr Gly Pro Pro Arg Ala Leu Glu Pro Pro Tyr Leu Pro Val Arg Ser  
325 330 335

Ser Asp Thr Pro Pro Pro Gly Gly Glu Arg Asn Gly Ala Gln Gln Gly  
340 345 350

Arg Leu Ser Val Gly Ser Val Tyr Arg Pro Asn Gln Asn Gly Arg Gly  
 355 360 365  
 Leu Pro Asp Leu Val Pro Asp Pro Asn Tyr Val Gln Ala Ser Thr Tyr  
 370 375 380  
 Val Gln Arg Ala His Leu Tyr Ser Leu Arg Cys Ala Ala Glu Glu Lys  
 385 390 395 400  
 Cys Leu Ala Ser Thr Ala Tyr Ala Pro Glu Ala Thr Asp Tyr Asp Val  
 405 410 415  
 Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln Gly Thr Ala  
 420 425 430  
 Asp Phe Leu Pro Asn Arg Pro Arg His Thr Trp Glu Trp His Ser Cys  
 435 440 445  
 His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr Asp Leu Leu  
 450 455 460  
 Asp Ala Ala Thr Gly Lys Lys Val Ala Glu Gly His Lys Ala Ser Phe  
 465 470 475 480  
 Cys Leu Glu Asp Ser Thr Cys Asp Phe Gly Asn Leu Lys Arg Tyr Ala  
 485 490 495  
 Cys Thr Ser His Thr Gln Gly Leu Ser Pro Gly Cys Tyr Asp Thr Tyr  
 500 505 510  
 Asn Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Gln Pro  
 515 520 525  
 Gly Asn Tyr Ile Leu Lys Val His Val Asn Pro Lys Tyr Ile Val Leu  
 530 535 540  
 Glu Ser Asp Phe Thr Asn Asn Val Val Arg Cys Asn Ile His Tyr Thr  
 545 550 555 560  
 Gly Arg Tyr Val Ser Ala Thr Asn Cys Lys Ile Val Gln Ser  
 565 570

<210> 16  
 <211> 774  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu  
 1 5 10 15  
 Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro His  
 20 25 30  
 Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln Pro Gln  
 35 40 45

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Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly Gln Lys  
50 55 60

Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly Gln Trp  
65 70 75 80

Gly Thr Val Cys Asp Asp Asp Phe Ser Ile His Ala Ala His Val Val  
85 90 95

Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala Ser Ser  
100 105 110

Ser Tyr Gly Lys Gly Glu Gly Pro Ile Trp Leu Asp Asn Leu His Cys  
115 120 125

Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly Trp Gly  
130 135 140

Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys Ser Asp  
145 150 155 160

Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile Asn Gln Ile  
165 170 175

Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala Ile Leu  
180 185 190

Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val Glu Val  
195 200 205

Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp Thr Ala  
210 215 220

Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly Glu Arg  
225 230 235 240

Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg Lys Gln  
245 250 255

Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala His Ile  
260 265 270

Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met Lys Asn  
275 280 285

Val Thr Cys Glu Asn Gly Leu Pro Ala Val Val Ser Cys Val Pro Gly  
290 295 300

Gln Val Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys Ala Tyr Lys  
305 310 315 320

Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Tyr Ile Gly Glu  
325 330 335

Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr Val Cys Asp  
340 345 350

Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg Glu Leu Gly  
355 360 365

Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly Gln Gly  
 370 375 380

Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn Glu Lys  
 385 390 395 400

Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys Asn His  
 405 410 415

Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly Leu Gln  
 420 425 430

Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly Arg Val  
 435 440 445

Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met Val Cys  
 450 455 460

Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg Gln Leu  
 465 470 475 480

Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr Trp His  
 485 490 495

Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys Cys Ser  
 500 505 510

Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu Asp Val  
 515 520 525

Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala Cys Ser  
 530 535 540

Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln Gln Thr  
 545 550 555 560

Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala Met Glu  
 565 570 575

Glu Asn Cys Leu Ser Ala Ser Ala Ala Gln Thr Asp Pro Thr Thr Gly  
 580 585 590

Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn Gly Gln  
 595 600 605

Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp His Asp  
 610 615 620

Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr Asp Leu  
 625 630 635 640

Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe  
 645 650 655

Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Asn Tyr Glu  
 660 665 670

Cys Ala Asn Phe Gly Asp Gln Gly Ile Thr Met Gly Cys Trp Asp Met  
 675 680 685

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Tyr	Arg	His	Asp	Ile	Asp	Cys	Gln	Trp	Val	Asp	Ile	Thr	Asp	Val	Pro
690						695					700				
Pro	Gly	Asp	Tyr	Leu	Phe	Gln	Val	Val	Ile	Asn	Pro	Asn	Phe	Glu	Val
705					710				715				720		
Ala	Glu	Ser	Asp	Tyr	Ser	Asn	Asn	Ile	Met	Lys	Cys	Arg	Ser	Arg	Tyr
						725			730				735		
Asp	Gly	His	Arg	Ile	Trp	Met	Tyr	Asn	Cys	His	Ile	Gly	Gly	Ser	Phe
						740		745				750			
Ser	Glu	Glu	Thr	Glu	Lys	Lys	Phe	Glu	His	Phe	Ser	Gly	Leu	Leu	Asn
						755		760				765			
Asn	Gln	Leu	Ser	Pro	Gln										
						770									

<210> 17  
<211> 754  
<212> PRT  
<213> Mus musculus

<400> 17															
Met	Arg	Ala	Val	Ser	Val	Trp	Tyr	Cys	Cys	Pro	Trp	Gly	Leu	Leu	Leu
1					5					10				15	
Leu	His	Cys	Leu	Cys	Ser	Phe	Ser	Val	Gly	Ser	Pro	Ser	Pro	Ser	Ile
					20			25					30		
Ser	Pro	Glu	Lys	Lys	Val	Gly	Ser	Gln	Gly	Leu	Arg	Phe	Arg	Leu	Ala
						35		40			45				
Gly	Phe	Pro	Arg	Lys	Pro	Tyr	Glu	Gly	Arg	Val	Glu	Ile	Gln	Arg	Ala
					50		55			60					
Gly	Glu	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Asp	Phe	Thr	Leu	Gln	Ala	Ala
					65		70			75			80		
His	Val	Leu	Cys	Arg	Glu	Leu	Gly	Phe	Thr	Glu	Ala	Thr	Gly	Trp	Thr
					85			90				95			
His	Ser	Ala	Lys	Tyr	Gly	Pro	Gly	Thr	Gly	Arg	Ile	Trp	Leu	Asp	Asn
					100			105			110				
Leu	Ser	Cys	Arg	Gly	Thr	Glu	Gly	Ser	Val	Thr	Glu	Cys	Ala	Ser	Arg
					115		120			125					
Gly	Trp	Gly	Asn	Ser	Asp	Cys	Thr	His	Asp	Glu	Asp	Ala	Gly	Val	Ile
					130		135			140					
Cys	Lys	Asp	Gln	Arg	Leu	Pro	Gly	Phe	Ser	Asp	Ser	Asn	Val	Ile	Glu
					145		150			155			160		
Val	Glu	His	Gln	Leu	Gln	Val	Glu	Glu	Val	Arg	Leu	Arg	Pro	Ala	Val
					165			170			175				
Glu	Trp	Gly	Arg	Arg	Pro	Leu	Pro	Val	Thr	Glu	Gly	Leu	Glu	Val	
					180			185			190				

Arg Leu Pro Glu Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala  
195 200 205

His Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Gly Glu Lys  
210 215 220

Arg Val Asn Met Ala Phe Tyr Arg Met Leu Ala Gln Lys Lys Gln His  
225 230 235 240

Ser Phe Gly Leu His Ser Val Ala Cys Val Gly Thr Glu Ala His Leu  
245 250 255

Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Thr Arg Cys  
260 265 270

Ser Gly Gly Asn Pro Ala Val Val Ser Cys Val Leu Gly Pro Leu Tyr  
275 280 285

Ala Thr Phe Thr Gly Gln Lys Lys Gln Gln His Ser Lys Pro Gln Gly  
290 295 300

Glu Ala Arg Val Arg Leu Lys Gly Gly Ala His Gln Gly Glu Gly Arg  
305 310 315 320

Val Glu Val Leu Lys Ala Gly Thr Trp Gly Thr Val Cys Asp Arg Lys  
325 330 335

Trp Asp Leu Gln Ala Ala Ser Val Val Cys Pro Glu Leu Gly Phe Gly  
340 345 350

Thr Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly  
355 360 365

Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Pro Ser Leu  
370 375 380

Trp Arg Cys Pro Ser Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser  
385 390 395 400

Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Val Glu Thr  
405 410 415

Lys Ile Arg Leu Ser Gly Gly Arg Ser Arg Tyr Glu Gly Arg Val Glu  
420 425 430

Val Gln Ile Gly Ile Pro Gly His Leu Arg Trp Gly Leu Ile Cys Gly  
435 440 445

Asp Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly  
450 455 460

Leu Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser  
465 470 475 480

Gly Asn Val Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Ser  
485 490 495

Glu Leu Ser Leu Asn Gln Cys Ala His His Ser Ser His Ile Thr Cys  
500 505 510

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Lys	Lys	Thr	Gly	Thr	Arg	Phe	Thr	Ala	Gly	Val	Ile	Cys	Ser	Glu	Thr
515								520						525	
Ala Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr															
530								535						540	
Ile	Glu	Asp	Arg	Pro	Leu	His	Met	Leu	Tyr	Cys	Ala	Ala	Glu	Glu	Asn
545								550						555	
Cys	Leu	Ala	Ser	Ser	Ala	Arg	Ser	Ala	Asn	Trp	Pro	Tyr	Gly	His	Arg
565								570						575	
Arg	Leu	Leu	Arg	Phe	Ser	Ser	Gln	Ile	His	Asn	Leu	Gly	Arg	Ala	Asp
580								585						590	
Phe	Arg	Pro	Lys	Ala	Gly	Arg	His	Ser	Trp	Val	Trp	His	Glu	Cys	His
595								600						605	
Gly	His	Tyr	His	Ser	Met	Asp	Ile	Phe	Thr	His	Tyr	Asp	Ile	Leu	Thr
610						615					620				
Pro	Asn	Gly	Thr	Lys	Val	Ala	Glu	Gly	His	Lys	Ala	Ser	Phe	Cys	Leu
625					630					635					640
Glu	Asp	Thr	Glu	Cys	Gln	Glu	Asp	Val	Ser	Lys	Arg	Tyr	Glu	Cys	Ala
645						650									655
Asn	Phe	Gly	Glu	Gln	Gly	Ile	Thr	Val	Gly	Cys	Trp	Asp	Leu	Tyr	Arg
660						665								670	
His	Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	Ile	Thr	Asp	Val	Lys	Pro	Gly
675						680								685	
Asn	Tyr	Ile	Leu	Gln	Val	Val	Ile	Asn	Pro	Asn	Phe	Glu	Val	Ala	Glu
690						695								700	
Ser	Asp	Phe	Thr	Asn	Asn	Ala	Met	Lys	Cys	Asn	Cys	Lys	Tyr	Asp	Gly
705						710								720	
His	Arg	Ile	Trp	Val	His	Asn	Cys	His	Ile	Gly	Asp	Ala	Phe	Ser	Glu
725								730						735	
Glu	Ala	Asn	Arg	Arg	Phe	Glu	Arg	Tyr	Pro	Gly	Gln	Thr	Ser	Asn	Gln
740						745								750	

Ile Val

<210> 18

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Copper-binding talon  
consensus sequence

<400> 18  
Trp Glu Trp His Ser Cys His Gln His Tyr His  
1 5 10

<210> 19  
<211> 451  
<212> PRT  
<213> Homo sapiens

<400> 19  
Met Glu Gln Trp Asp His Phe His Asn Gln Gln Glu Asp Thr Asp Ser  
1 5 10 15

Cys Ser Glu Ser Val Lys Phe Asp Ala Arg Ser Met Thr Ala Leu Leu  
20 25 30

Pro Pro Asn Pro Lys Asn Ser Pro Ser Leu Gln Glu Lys Leu Lys Ser  
35 40 45

Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu Val Phe Ala Val Leu  
50 55 60

Ile Pro Leu Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp Glu Thr  
65 70 75 80

Lys Asn Cys Ser Val Ser Ser Thr Asn Ala Asn Asp Ile Thr Gln Ser  
85 90 95

Leu Thr Gly Lys Gly Asn Asp Ser Glu Glu Glu Met Arg Phe Gln Glu  
100 105 110

Val Phe Met Glu His Met Ser Asn Met Glu Lys Arg Ile Gln His Ile  
115 120 125

Leu Asp Met Glu Ala Asn Leu Met Asp Thr Glu His Phe Gln Asn Phe  
130 135 140

Ser Met Thr Thr Asp Gln Arg Phe Asn Asp Ile Leu Leu Gln Leu Ser  
145 150 155 160

Thr Leu Phe Ser Ser Val Gln Gly His Gly Asn Ala Ile Asp Glu Ile  
165 170 175

Ser Lys Ser Leu Ile Ser Leu Asn Thr Thr Leu Leu Asp Leu Gln Leu  
180 185 190

Asn Ile Glu Asn Leu Asn Gly Lys Ile Gln Glu Asn Thr Phe Lys Gln  
195 200 205

Gln Glu Glu Ile Ser Lys Leu Glu Glu Arg Val Tyr Asn Val Ser Ala  
210 215 220

Glu Ile Met Ala Met Lys Glu Glu Gln Val His Leu Glu Gln Glu Ile  
225 230 235 240

Lys Gly Glu Val Lys Val Leu Asn Asn Ile Thr Asn Asp Leu Arg Leu  
245 250 255

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Lys	Asp	Trp	Glu	His	Ser	Gln	Thr	Leu	Arg	Asn	Ile	Thr	Leu	Ile	Gln
260							265						270		
Gly	Pro	Pro	Gly	Pro	Pro	Gly	Glu	Lys	Gly	Asp	Arg	Gly	Pro	Thr	Gly
275							280					285			
Glu	Ser	Gly	Pro	Arg	Gly	Phe	Pro	Gly	Pro	Ile	Gly	Pro	Pro	Gly	Leu
290							295					300			
Lys	Gly	Asp	Arg	Gly	Ala	Ile	Gly	Phe	Pro	Gly	Ser	Arg	Gly	Leu	Pro
305							310					315			320
Gly	Tyr	Ala	Gly	Arg	Pro	Gly	Asn	Ser	Gly	Pro	Lys	Gly	Gln	Lys	Gly
325							330					335			
Glu	Lys	Gly	Ser	Gly	Asn	Thr	Leu	Thr	Pro	Phe	Thr	Lys	Val	Arg	Leu
340							345					350			
Val	Gly	Gly	Ser	Gly	Pro	His	Glu	Gly	Arg	Val	Glu	Ile	Leu	His	Ser
355							360					365			
Gly	Gln	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Arg	Trp	Glu	Val	Arg	Val	Gly
370							375					380			
Gln	Val	Val	Cys	Arg	Ser	Leu	Gly	Tyr	Pro	Gly	Val	Gln	Ala	Val	His
385							390					395			400
Lys	Ala	Ala	His	Phe	Gly	Gln	Gly	Thr	Gly	Pro	Ile	Trp	Leu	Asn	Glu
405							410					415			
Val	Phe	Cys	Phe	Gly	Arg	Glu	Ser	Ser	Ile	Glu	Glu	Cys	Lys	Ile	Arg
420							425					430			
Gln	Trp	Gly	Thr	Arg	Ala	Cys	Ser	His	Ser	Glu	Asp	Ala	Gly	Val	Thr
435							440					445			
Cys	Thr	Leu													
		450													

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 20  
gcttaccaag aaacccatgt cagc 24

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 21		
ggcagttagt caggtgctgc		20
<210> 22		
<211> 981		
<212> DNA		
<213> Mus musculus		
<220>		
<221> CDS		
<222> (107)..(748)		
<400> 22		
gaattcggca cgagggccgg caccggcgcc ccaccccgac ctcaaactgc agtccggcgc	60	
cgcggggcag gacaagggaa aggaataaac acgtttggtg agagcc atg gca ctc	115	
Met Ala Leu		
1		
aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc	163	
Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe		
5 10 15		
cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg	211	
Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg		
20 25 30 35		
cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag	259	
Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln		
40 45 50		
tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg	307	
Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly		
55 60 65		
gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac	355	
Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp		
70 75 80		
tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac	403	
Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn		
85 90 95		
cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg	451	
Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly		
100 105 110 115		
gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa	499	
Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln		
120 125 130		
gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca	547	
Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Tyr Glu Pro		
135 140 145		
cac tgt acc agc aag gtg aac ctt gtg aag atc tcc tcc acc gtc tcc	595	
His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser Thr Val Ser		
150 155 160		

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agc cct cggtt gac acg gctt gctt gcc gtc atc tgc agt gct ctg gcc	643
Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala	
165	170
	175

acg gtg ctg ctc gcc ctg ctc atc ctg tgt gtc atc tac tgc aag agg	691
Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr Cys Lys Arg	
180	185
	190
	195

cag ttc atg gag aag aaa ccc agc tgt aag ctc cca tcc ctc tgt ctc	739
Gln Phe Met Glu Lys Lys Pro Ser Cys Lys Leu Pro Ser Leu Cys Leu	
200	205
	210

act gtg aag tgtagcttggtt agcattgtca cccaagagtt ctcaagacac	788
Thr Val Lys	

ctggctgaga cctaagacct ttagagcatc aacagctact tagaatacaa gatgcaggaa	848
aacgagccctc ttccatggaaatc tcaggccctc ctatggatgc tggcaaggct gtgtatgtctc	908
aaggctacca ggaaaaaaaata aaagttgtct ataccctaaa aaaaaaaaaaaa aaaaaaaaaaaa	968
aacatgcggc cgc	981

<210> 23

<211> 214

<212> PRT

<213> Mus musculus

<400> 23

Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala	
1	5
	10
	15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly	
20	25
	30

Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu	
35	40
	45

Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe	
50	55
	60

Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe	
65	70
	75
	80

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala	
85	90
	95

Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala	
100	105
	110

Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val	
115	120
	125

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro	
130	135
	140

Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser	
145	150
	155
	160

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Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser  
 165 170 175  
 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr  
 180 185 190  
 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Cys Lys Leu Pro Ser  
 195 200 205  
 Leu Cys Leu Thr Val Lys  
 210

&lt;210&gt; 24

&lt;211&gt; 642

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(642)

&lt;400&gt; 24

atg gca ctc aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc	48
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala	
1 5 10 15	

att ctc ttc cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga	96
Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly	
20 25 30	

gat tgc agg cag cag gaa ttc aag gat cga tct gga aac tgc ctc	144
Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu	
35 40 45	

tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc	192
Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe	
50 55 60	

ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc	240
Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe	
65 70 75 80	

aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg	288
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala	
85 90 95	

ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct	336
Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala	
100 105 110	

gtc tgc ggg gac tgc ctc gca gga ttt tac cgg aag acc aaa ctg gtt	384
Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val	
115 120 125	

ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc	432
Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro	
130 135 140	

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tac gaa cca cac tgt acc agc aag gtg aac ctt gtg aag atc tcc tcc	480
Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser	
145 150 155 160	
acc gtc tcc agc cct cgg gac acg gcg ctg gct gcc gtc atc tgc agt	528
Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Val Ile Cys Ser	
165 170 175	
gct ctg gcc acg gtg ctg ctc gcc ctg ctc atc ctg tgt gtc atc tac	576
Ala Leu Ala Thr Val Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr	
180 185 190	
tgc aag agg cag ttc atg gag aag aaa ccc agc tgt aag ctc cca tcc	624
Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Cys Lys Leu Pro Ser	
195 200 205	
ctc tgt ctc act gtg aag	642
Leu Cys Leu Thr Val Lys	
210	

&lt;210&gt; 25

&lt;211&gt; 555

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(555)

&lt;400&gt; 25

gaa acc gga gat tgc agg cag cag gaa ttc aag gat cga tct gga aac	48
Glu Thr Gly Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn	
1 5 10 15	

tgt gtc ctc tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa	96
Cys Val Leu Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu	
20 25 30	

tgt ggc ttc ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg	144
Cys Gly Phe Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro	
35 40 45	

cac cgg ttc aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg	192
His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala	
50 55 60	

gac tgt gcg ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc	240
Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr	
65 70 75 80	

agt gat gct gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc	288
Ser Asp Ala Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr	
85 90 95	

aaa ctg gtt ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca	336
Lys Leu Val Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro	
100 105 110	

- 34 -

cct cct ccc tac gaa cca cac tgt acc agc aag gtg aac ctt gtg aag	384
Pro Pro Pro Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys	
115 120 125	
atc tcc tcc acc gtc tcc agc cct cgg gac acg gcg ctg gct gcc gtc	432
Ile Ser Ser Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val	
130 135 140	
atc tgc agt gct ctg gcc acg gtg ctg ctc gcc ctg ctc atc ctg tgt	480
Ile Cys Ser Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys	
145 150 155 160	
gtc atc tac tgc aag agg cag ttc atg gag aag aaa ccc agc tgt aag	528
Val Ile Tyr Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Cys Lys	
165 170 175	
ctc cca tcc ctc tgt ctc act gtg aag	555
Leu Pro Ser Leu Cys Leu Thr Val Lys	
180 185	

<210> 26  
<211> 655  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (110)..(559)

<400> 26  
gaattcggca cgagggcggtt tggcgcgaaa gtgttaccaa gctgcggaaa gcgtgagtct 60  
ggagcacacgc actggcgagt agcaggaata aacacgtttt gtgagagcc atg gca ctc 118  
Met Ala Leu  
1

aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc	166
Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe	
5 10 15	

cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg	214
Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg	
20 25 30 35	

cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag	262
Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln	
40 45 50	

tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg	310
Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly	
55 60 65	

gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac	358
Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp	
70 75 80	

tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac	406
Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn	
85 90 95	

cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg 454  
 Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly  
 100 105 110 115  
  
 gac tgc ctg cca gga ttt tac cg<sup>g</sup> aag acc aaa ctg gtt ggt ttt caa 502  
 Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln  
 120 125 130  
  
 gac atg gag tgt gtg ccc tgc gga gac cca cct ccc tac gaa cca 550  
 Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Tyr Glu Pro  
 135 140 145  
  
 cac tgt gag tgatgtgcca agtggcagca gac<sup>c</sup>ttaaaa aaaaaaaagaa 599  
 His Cys Glu  
 150  
  
 aaaaaaaaaacaa acaaaaaacaa aaaaaaaaaaa aaaaaaaaaaa aaatttccgc ggccgc 655

<210> 27  
 <211> 150  
 <212> PRT  
 <213> Mus musculus

<400> 27  
 Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala  
 1 5 10 15  
  
 Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly  
 20 25 30  
  
 Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu  
 35 40 45  
  
 Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe  
 50 55 60  
  
 Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe  
 65 70 75 80  
  
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala  
 85 90 95  
  
 Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala  
 100 105 110  
  
 Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val  
 115 120 125  
  
 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro  
 130 135 140  
  
 Tyr Glu Pro His Cys Glu  
 145 150

<210> 28  
<211> 450  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (1)..(450)

<400> 28

atg	gca	ctc	aag	gtc	cta	cct	cta	cac	agg	acg	gtg	ctc	ttc	gct	gcc	48
Met	Ala	Leu	Lys	Val	Leu	Pro	Leu	His	Arg	Thr	Val	Leu	Phe	Ala	Ala	
1	5				10				15							

att ctc ttc cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga 96

Ile	Leu	Phe	Leu	Leu	His	Leu	Ala	Cys	Lys	Val	Ser	Cys	Glu	Thr	Gly	
			20			25			30							

gat tgc agg cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc 144

Asp	Cys	Arg	Gln	Gln	Glu	Phe	Lys	Asp	Arg	Ser	Gly	Asn	Cys	Val	Leu	
			35		40				45							

tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc 192

Cys	Lys	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	
	50			55			60									

ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc 240

Gly	Tyr	Gly	Glu	Asp	Ala	Gln	Cys	Val	Pro	Cys	Arg	Pro	His	Arg	Phe	
	65		70			75			80							

aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg 288

Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Ala	Asp	Cys	Ala	
	85			90			95									

ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct 336

Leu	Val	Asn	Arg	Phe	Gln	Arg	Ala	Asn	Cys	Ser	His	Thr	Ser	Asp	Ala	
	100			105			110									

gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt 384

Val	Cys	Gly	Asp	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	
	115				120			125								

ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc 432

Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	
	130			135			140									

tac gaa cca cac tgt gag 450

Tyr	Glu	Pro	His	Cys	Glu											
	145			150												

<210> 29  
<211> 363  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (1)..(363)

<400> 29  
gaa acc gga gat tgc agg cag cag gaa ttc aag gat cga tct gga aac 48  
Glu Thr Gly Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn  
1 5 10 15

tgt gtc ctc tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa 96  
Cys Val Leu Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu  
20 25 30

tgt ggc ttc ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg 144  
Cys Gly Phe Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro  
35 40 45

cac cgg ttc aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg 192  
His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala  
50 55 60

gac tgt gcg ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc 240  
Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr  
65 70 75 80

agt gat gct gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc 288  
Ser Asp Ala Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr  
85 90 95

aaa ctg gtt ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca 336  
Lys Leu Val Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro  
100 105 110

cct cct ccc tac gaa cca cac tgt gag 363  
Pro Pro Pro Tyr Glu Pro His Cys Glu  
115 120

<210> 30  
<211> 272  
<212> PRT  
<213> Mus musculus

<400> 30  
Met Tyr Val Trp Val Gln Gln Pro Thr Ala Leu Leu Leu Leu Ala Leu  
1 5 10 15

Thr Leu Gly Val Thr Ala Arg Arg Leu Asn Cys Val Lys His Thr Tyr  
20 25 30

Pro Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met  
35 40 45

Val Ser Arg Cys Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu  
50 55 60

Thr Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys  
65 70 75 80

Thr Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr  
85 90 95

Pro Thr Gln Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg  
100 105 110

Gln Asp Ser Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro  
 115 120 125

Gly His Phe Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn  
 130 135 140

Cys Thr Leu Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu  
 145 150 155 160

Asp Ala Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu  
 165 170 175

Thr Gln Arg Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val  
 180 185 190

Trp Pro Arg Thr Ser Glu Leu Pro Ser Pro Pro Thr Leu Val Thr Pro  
 195 200 205

Glu Gly Pro Ala Phe Ala Val Leu Leu Gly Leu Gly Leu Gly Leu Leu  
 210 215 220 .

Ala Pro Leu Thr Val Leu Leu Ala Leu Tyr Leu Leu Arg Lys Ala Trp  
 225 230 235 240

Arg Leu Pro Asn Thr Pro Lys Pro Cys Trp Gly Asn Ser Phe Arg Thr  
 245 250 255

Pro Ile Gln Glu Glu His Thr Asp Ala His Phe Thr Leu Ala Lys Ile  
 260 265 270

<210> 31  
<211> 1344  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (273)..(1022)

<400> 31  
gaattcgaa cgagggaaac ctaatttcc tgaggctgag ggagggtgga gggctcaag 60  
gcaacgctgg ccccacgacg gagtgccagg agcactaaca gtacccttag cttgccttcc 120  
tcctccctcc ttttatattt caagttcattt ttatattctc cttgcgtaac aaccttcttc 180  
ccttctgcac cactgccgt acccttaccc gccccgccac ctcccttgcta ccccaacttt 240  
gaaaccacag ctgttggcag ggtcccccagc tc atg cca gcc tca tct cct ttc 293  
Met Pro Ala Ser Ser Pro Phe  
1 5

ttg cta gcc ccc aaa ggg cct cca ggc aac atg ggg ggc cca gtc aga 341  
Leu Leu Ala Pro Lys Gly Pro Pro Gly Asn Met Gly Gly Pro Val Arg  
10 15 20

gag ccg gca ctc tca gtt gcc ctc tgg ttg agt tgg ggg gca gct ctg Glu Pro Ala Leu Ser Val Ala Leu Trp Leu Ser Trp Gly Ala Ala Leu	389
25 30 35	
ggg gcc gtg gct tgt gcc atg gct ctg ctg acc caa caa aca gag ctg Gly Ala Val Ala Cys Ala Met Ala Leu Leu Thr Gln Gln Thr Glu Leu	437
40 45 50 55	
cag agc ctc agg aga gag gtg agc cgg ctg cag ggg aca gga ggc ccc Gln Ser Leu Arg Arg Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro	485
60 65 70	
tcc cag aat ggg gaa ggg tat ccc tgg cag agt ctc ccg gag cag agt Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser	533
75 80 85	
tcc gat gcc ctg gaa gcc tgg gag aat ggg gag aga tcc cgg aaa agg Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg	581
90 95 100	
aga gca gtg ctc acc caa aaa cag aag cag cac tct gtc ctg cac Arg Ala Val Leu Thr Gln Lys Gln Lys Gln His Ser Val Leu His	629
105 110 115	
ctg gtt ccc att aac gcc acc tcc aag gat gac tcc gat gtg aca gag Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp Ser Asp Val Thr Glu	677
120 125 130 135	
gtg atg tgg caa cca gct ctt agg cgt ggg aga ggc cta cag gcc caa Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln	725
140 145 150	
gga tat ggt gtc cga atc cag gat gct gga gtt tat ctg ctg tat agc Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser	773
155 160 165	
cag gtc ctg ttt caa gac gtg act ttc acc atg ggt cag gtg gtg tct Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln Val Val Ser	821
170 175 180	
cga gaa ggc caa gga agg cag gag act cta ttc cga tgt ata aga agt Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser	869
185 190 195	
atg ccc tcc cac ccg gac cgg gcc tac aac agc tgc tat agc gca ggt Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly	917
200 205 210 215	
gtc ttc cat tta cac caa ggg gat att ctg agt gtc ata att ccc cgg Val Phe His Leu His Gln Gly Asp Ile Leu Ser Val Ile Ile Pro Arg	965
220 225 230	
gca agg gcg aaa ctt aac ctc tct cca cat gga acc ttc ctg ggg ttt Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly Thr Phe Leu Gly Phe	1013
235 240 245	
gtg aaa ctg tgattgtgtt ataaaaagtg gctcccagct tggaaagacca Val Lys Leu	1062
250	

gggtgggtac atactggaga cagccaagag ctgagtatat aaaggagagg gaatgtgcag 1122  
 gaacagaggc atcttcctgg gtttggctcc ccgttcctca cttttccctt ttcattccca 1182  
 ccccctagac tttgattta cgatatac tt gcttctgttc cccatggagc tccgaattct 1242  
 tgcgtgtgtg tagatgaggg gcgggggacg ggcgccaggc attgttcaga cctggtcggg 1302  
 gcccactgga agcatccaga acagcaccac catctagcgg cc 1344

<210> 32  
<211> 250  
<212> PRT  
<213> Homo sapiens

<400> 32  
Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly  
1 5 10 15  
Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp  
20 25 30  
Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu  
35 40 45  
Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg  
50 55 60  
Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp  
65 70 75 80  
Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn  
85 90 95  
Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys  
100 105 110  
Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys  
115 120 125  
Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg  
130 135 140  
Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala  
145 150 155 160  
Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe  
165 170 175  
Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr  
180 185 190  
Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr  
195 200 205  
Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile  
210 215 220

Leu	Ser	Val	Ile	Ile	Pro	Arg	Ala	Arg	Ala	Lys	Leu	Asn	Leu	Ser	Pro
225					230					235					240
His	Gly	Thr	Phe	Leu	Gly	Phe	Val	Lys	Leu						
							245			250					

<210> 33  
<211> 754  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> (1)..(750)

<400> 33

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atg cca gcc tca tct cct ttc ttg cta gcc ccc aaa ggg cct cca ggc 48
Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
          1           5           10          15

```

```

aac atg ggg ggc cca gtc aga gag ccg gca ctc tca gtt gcc ctc tgg 96
Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
          20           25           30

```

```

ttg agt tgg ggg gca gct ctg ggg gcc gtg gct tgt gcc atg gct ctg      144
Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
                         35          40          45

```

ctg acc caa caa aca gag ctg cag agc ctc agg aga gag gtg agc cg 192  
 Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg  
       50                 55                 60

ctg cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg tat ccc tgg 240  
 Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp  
     65                70                75                80

```

cag agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc tgg gag aat      288
Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn
                         85          90          95

```

ggg gag aga tcc cg<sup>g</sup> aaa agg aga gca gtg ctc acc caa aaa cag aag 336  
 Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys  
 100 105 110

aag cag cac tct gtc ctg cac ctg gtt ccc att aac gcc acc tcc aag	384
Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys	
115 120 125	

```

gat gac tcc gat gtg aca gag gtg atg tgg caa cca gct ctt agg cgt      432
Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg
   130          135          140

```

ggg aga ggc cta cag gcc caa gga tat ggt gtc cga atc cag gat gct 480  
 Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala  
 145 150 155 160

```

gga gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac gtg act ttc      528
Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe
165          170          175

```

acc atg ggt cag gtg gtg tct cga gaa ggc caa gga agg cag gag act	576
Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr	
180	185
185	190
cta ttc cga tgt ata aga agt atg ccc tcc cac ccg gac cg <sup>g</sup> gcc tac	624
Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr	
195	200
200	205
aac agc tgc tat agc gca ggt gtc ttc cat tta cac caa ggg gat att	672
Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile	
210	215
215	220
ctg agt gtc ata att ccc cgg gca agg qc <sup>g</sup> aaa ctt aac ctc tct cca	720
Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro	
225	230
230	235
235	240
cat gga acc ttc ctg ggg ttt gtg aaa ctg tgat	754
His Gly Thr Phe Leu Gly Phe Val Lys Leu	
245	250

<210> 34  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 34  
Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu  
1                   5                   10                   15  
Phe

<210> 35  
<211> 49  
<212> PRT  
<213> Homo sapiens

<400> 35  
Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly  
1                   5                   10                   15  
Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp  
20                   25                   30  
Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu  
35                   40                   45

Leu

<210> 36  
<211> 603  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(603)

<400> 36  
 acc caa caa aca gag ctg cag agc ctc agg aga gag gtg agc cg<sub>g</sub> ctg 48  
 Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg Leu  
 1 5 10 15  
  
 cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg tat ccc tgg cag 96  
 Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln  
 20 25 30  
  
 agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc tgg gag aat ggg 144  
 Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly  
 35 40 45  
  
 gag aga tcc cgg aaa agg aga gca gtg ctc acc caa aaa cag aag aag 192  
 Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys  
 50 55 60  
  
 cag cac tct gtc ctg cac ctg gtt ccc att aac gcc acc tcc aag gat 240  
 Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp  
 65 70 75 80  
  
 gac tcc gat gtg aca gag gtg atg tgg caa cca gct ctt agg cgt ggg 288  
 Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly  
 85 90 95  
  
 aga ggc cta cag gcc caa gga tat ggt gtc cga atc cag gat gct gga 336  
 Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly  
 100 105 110  
  
 gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac gtg act ttc acc 384  
 Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr  
 115 120 125  
  
 atg ggt cag gtg gtg tct cga gaa ggc caa gga agg cag gag act cta 432  
 Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu  
 130 135 140  
  
 ttc cga tgt ata aga agt atg ccc tcc cac ccg gac cgg gcc tac aac 480  
 Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn  
 145 150 155 160  
  
 agc tgc tat agc gca ggt gtc ttc cat tta cac caa ggg gat att ctg 528  
 Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu  
 165 170 175  
  
 agt gtc ata att ccc cgg gca agg gcg aaa ctt aac ctc tct cca cat 576  
 Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His  
 180 185 190  
  
 gga acc ttc ctg ggg ttt gtg aaa ctg 603  
 Gly Thr Phe Leu Gly Phe Val Lys Leu  
 195 200

- 44 -

<210> 37  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 37

Thr	Gln	Gln	Thr	Glu	Leu	Gln	Ser	Leu	Arg	Arg	Glu	Val	Ser	Arg	Leu
1				5				10						15	

Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln

		20			25				30						
--	--	----	--	--	----	--	--	--	----	--	--	--	--	--	--

Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly

		35			40				45						
--	--	----	--	--	----	--	--	--	----	--	--	--	--	--	--

Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys

		50			55				60						
--	--	----	--	--	----	--	--	--	----	--	--	--	--	--	--

Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp

		65			70				75				80		
--	--	----	--	--	----	--	--	--	----	--	--	--	----	--	--

Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly

		85			90				95						
--	--	----	--	--	----	--	--	--	----	--	--	--	--	--	--

Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly

		100			105				110						
--	--	-----	--	--	-----	--	--	--	-----	--	--	--	--	--	--

Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr

		115			120				125						
--	--	-----	--	--	-----	--	--	--	-----	--	--	--	--	--	--

Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu

		130			135				140						
--	--	-----	--	--	-----	--	--	--	-----	--	--	--	--	--	--

Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn

		145			150				155				160		
--	--	-----	--	--	-----	--	--	--	-----	--	--	--	-----	--	--

Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu

		165			170				175						
--	--	-----	--	--	-----	--	--	--	-----	--	--	--	--	--	--

Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His

		180			185				190						
--	--	-----	--	--	-----	--	--	--	-----	--	--	--	--	--	--

Gly Thr Phe Leu Gly Phe Val Lys Leu

		195			200										
--	--	-----	--	--	-----	--	--	--	--	--	--	--	--	--	--

<210> 38  
<211> 699  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(699)

<400> 38

atg	ggg	ggc	cca	gtc	aga	gag	ccg	gca	ctc	tca	gtt	gcc	ctc	tgg	ttg	48
1																

Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp Leu

			5					10				15				
--	--	--	---	--	--	--	--	----	--	--	--	----	--	--	--	--

- 45 -

agt tgg ggg gca gct ctg ggg gcc gtg gct tgt gcc atg gct ctg ctg	96
Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu Leu	
20	25
30	
acc caa caa aca gag ctg cag agc ctc agg aga gag gtg agc cgg ctg	144
Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg Leu	
35	40
45	
cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg tat ccc tgg cag	192
Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln	
50	55
60	
agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc tgg gag aat ggg	240
Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly	
65	70
75	80
gag aga tcc cgg aaa agg aga gca gtg ctc acc caa aaa cag aag aag	288
Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys	
85	90
95	
cag cac tct gtc ctg cac ctg gtt ccc att aac gcc acc tcc aag gat	336
Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp	
100	105
110	
gac tcc gat gtg aca gag gtg atg tgg caa cca gct ctt agg cgt ggg	384
Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly	
115	120
125	
aga ggc cta cag gcc caa gga tat ggt gtc cga atc cag gat gct gga	432
Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly	
130	135
140	
gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac gtg act ttc acc	480
Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr	
145	150
155	160
atg ggt cag gtg tct cga gaa ggc caa gga agg cag gag act cta	528
Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu	
165	170
175	
ttc cga tgt ata aga agt atg ccc tcc cac ccg gac cgg gcc tac aac	576
Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn	
180	185
190	
agc tgc tat agc gca ggt gtc ttc cat tta cac caa ggg gat att ctg	624
Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu	
195	200
205	
agt gtc ata att ccc cgg gca agg gcg aaa ctt aac ctc tct cca cat	672
Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His	
210	215
220	
gga acc ttc ctg ggg ttt gtg aaa ctg	699
Gly Thr Phe Leu Gly Phe Val Lys Leu	
225	230

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<210> 39  
<211> 233  
<212> PRT  
<213> Homo sapiens

<400> 39  
Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp Leu  
1 5 10 15

Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu Leu  
20 25 30

Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg Leu  
35 40 45

Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln  
50 55 60

Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly  
65 70 75 80

Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys  
85 90 95

Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp  
100 105 110

Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly  
115 120 125

Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly  
130 135 140

Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr  
145 150 155 160

Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu  
165 170 175

Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn  
180 185 190

Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu  
195 200 205

Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His  
210 215 220

Gly Thr Phe Leu Gly Phe Val Lys Leu  
225 230

<210> 40  
<211> 615  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(615)

<400> 40  
atg gct ctg ctg acc caa aca gag ctg cag agc ctc agg aga gag 48  
Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu  
1 5 10 15

gtg agc cg<sup>g</sup> ctg cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg 96  
Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly  
20 25 30

tat ccc tgg cag agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc 144  
Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala  
35 40 45

tgg gag aat ggg gag aga tcc cg<sup>g</sup> aaa agg aga gca gtg ctc acc caa 192  
Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln  
50 55 60

aaa cag aag aag cag cac tct gtc ctg cac ctg gtt ccc att aac gcc 240  
Lys Gln Lys Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala  
65 70 75 80

acc tcc aag gat gac tcc gat gtg aca gag gtg atg tgg caa cca gct 288  
Thr Ser Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala  
85 90 95

ctt agg cgt ggg aga ggc cta cag gcc caa gga tat ggt gtc cga atc 336  
Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile  
100 105 110

cag gat gct gga gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac 384  
Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp  
115 120 125

gtg act ttc acc atg ggt cag gtg gtg tct cga gaa ggc caa gga agg 432  
Val Thr Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg  
130 135 140

cag gag act cta ttc cga tgt ata aga agt atg ccc tcc cac ccg gac 480  
Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp  
145 150 155 160

cgg gcc tac aac agc tgc tat agc gca ggt gtc ttc cat tta cac caa 528  
Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln  
165 170 175

ggg gat att ctg agt gtc ata att ccc cgg gca agg ggc aaa ctt aac 576  
Gly Asp Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn  
180 185 190

ctc tct cca cat gga acc ttc ctg ggg ttt gtg aaa ctg 615  
Leu Ser Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu  
195 200 205

<210> 41  
<211> 205  
<212> PRT  
<213> Homo sapiens

<400> 41  
Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu  
1 5 10 15  
  
Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly  
20 25 30  
  
Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala  
35 40 45  
  
Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln  
50 55 60  
  
Lys Gln Lys Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala  
65 70 75 80  
  
Thr Ser Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala  
85 90 95  
  
Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile  
100 105 110  
  
Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp  
115 120 125  
  
Val Thr Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg  
130 135 140  
  
Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp  
145 150 155 160  
  
Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln  
165 170 175  
  
Gly Asp Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn  
180 185 190  
  
Leu Ser Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu  
195 200 205

&lt;210&gt; 42

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Consensus sequence

&lt;220&gt;

&lt;223&gt; Xaas at position 2, 4-6, 12, 13 and 16 may be any amino acid

&lt;220&gt;

&lt;223&gt; Any 2 of the Xaas at positions 4-6 may be absent, intended to equal a range of 1-3;

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<220>

<223> Any 1 of the Xaa at positions 12-13 may be absent,  
intended to equal a range of 1-2;

<400> 42

Val Xaa Ile Xaa Xaa Xaa Gly Val Tyr Leu Leu Xaa Xaa Glu Val Xaa  
1 5 10 15

Phe

<210> 43

<211> 233

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala  
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe  
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe  
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro  
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser  
65 70 75 80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro  
85 90 95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu  
100 105 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser  
115 120 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly  
130 135 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala  
145 150 155 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro  
165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu  
180 185 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu  
195 200 205

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Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly  
210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu  
225 230

<210> 44  
<211> 249  
<212> PRT  
<213> Homo sapiens

<400> 44  
Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg Gly Glu Pro  
1 5 10 15

Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly Leu Ala Leu  
20 25 30

Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly Ser Arg Ala  
35 40 45

Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val Ala Glu Glu  
50 55 60

Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu Ser Gln Asp  
65 70 75 80

Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg Ser Ala Pro  
85 90 95

Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala His Tyr Glu  
100 105 110

Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly Val Asp Gly  
115 120 125

Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn Ser Ser Ser Pro Leu  
130 135 140

Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg Ala Gly Leu  
145 150 155 160

Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys Ala Val Tyr  
165 170 175

Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu Arg Cys Leu  
180 185 190

Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro Gln Leu Arg  
195 200 205

Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly Ser Ser Leu  
210 215 220

Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala Pro Phe Leu  
225 230 235 240

Thr Tyr Phe Gly Leu Phe Gln Val His  
245

<210> 45  
 <211> 1119  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (140)..(871)

<400> 45  
 gtcgaccac gcgtccggca ggtatgttgc agtgtcgcbc ccagggctct gagactgagc 60  
 ctgccatcca ctcgcacgccc tttctttcag ggctttcgg ctgttgctta cactgatgtg 120  
 accccccctcc ctttttgga atg atg ggg atc ttt ttg gtg tat gtt gga ttt 172  
                   Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe  
                   1               5                  10

gtt ttc ttt tcc gtt tta tat gta caa caa ggg ctt tct tct caa gca 220  
 Val Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala  
                   15               20                  25

aaa ttt acc gag ttt ccg cgg aac gtg acg gcg acc gag ggg cag aat 268  
 Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn  
                   30               35                  40

gtg gag atg tcc tgc gcc ttc cag agc ggc tcc gcc tcg gtg tat ctg 316  
 Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu  
                   45               50                  55

gag atc caa tgg tgg ttc ctg cgg ggg ccg gag gac ctg gat ccc ggg 364  
 Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly  
                   60               65                  70                  75

gcc gag ggg gcc ggc gcg cag gtg gag ctc ttg ccc gac aga gac ccg 412  
 Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro  
                   80               85                  90

gac agc gac ggg acc aag atc agc aca gtg aaa gtc caa ggc aat gac 460  
 Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp  
                   95               100                  105

atc tcc cac aag ctt cag att tcc aaa gtg agg aaa aag gat gaa ggc 508  
 Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly  
                   110               115                  120

tta tat gag tgc agg gtg act gat gcc aac tac ggg gag ctt cag gaa 556  
 Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu  
                   125               130                  135

cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat gcc cgc 604  
 His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg  
                   140               145                  150                  155

aga atg cag gcc ttc gaa gcc tcg ccc atg tgg ctg cag gat atg aag 652  
 Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys  
                   160               165                  170

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ccc cgc aag aac gtc tcc gca gcc atc ccc agc agc atc cat ggc tct	700
Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser	
175	180
185	
gcc aac caa cga acg cac tcc acc tcc agc cct caa gtg gta gcc aaa	748
Ala Asn Gln Arg Thr His Ser Thr Ser Pro Gln Val Val Ala Lys	
190	195
200	
atc ccc aaa caa agt cca caa tca ggt atg gaa acc cat ttc gag cct	796
Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro	
205	210
215	
ttt att tta cca ctc aca aac gct cca cag aaa ggt cag tcg tat aga	844
Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg	
220	225
230	235
gta gac aga ttt atg aat ggt gat ttt taaaatcgga gaccctaggc	891
Val Asp Arg Phe Met Asn Gly Asp Phe	
240	
agtgcaggat attatgagag gtgagcactg agcctgcacc aattcactca gagctcaaag	951
catgtgggtg caccgggtca gtccccctagt ggtgcattcat ttccaggggca tctgagagct	1011
ggactctggc ttttatcattt tctgtattta cacattataa gaacaataaa tcatgtaatg	1071
ttggttacat tacaaaaaaaaaaaaaaa aaaaaaaaaaaaaagg gcggccgc	1119
<210> 46	
<211> 244	
<212> PRT	
<213> Homo sapiens	
<400> 46	
Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe Val Phe Phe Ser Val	
1	5
10	15
Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Phe	
20	25
30	
Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys	
35	40
45	
Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp	
50	55
60	
Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly Ala Glu Gly Ala Gly	
65	70
75	80
Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Ser Asp Gly Thr	
85	90
95	
Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu	
100	105
110	
Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg	
115	120
125	

<210> 47  
<211> 735  
<212> DNA  
<213> *Homo sapien*

<220>  
<221> CDS  
<222> (1)..(732)

<400> 47  
atg atg ggg atc ttt ttg gtg tat gtt gga ttt gtt ttc ttt tcc gtt 48  
Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe Val Phe Phe Ser Val  
1 5 10 15

tta tat gta caa caa ggg ctt tct tct caa gca aaa ttt acc gag ttt 96  
 Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Phe  
           20                 25                 30

ccg cg aac gtg acg gcg acc gag ggg cag aat gtg gag atg tcc tgc 144  
 Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys  
 35 40 45

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gcc ttc cag agc ggc tcc gcc tcg gtg tat ctg gag atc caa tgg tgg 192
Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp
      50           55           60

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ttc ctg cgg ggg ccg gag gac ctg gat ccc ggg gcc gag ggg gcc ggc 240  
 Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly Ala Glu Gly Ala Gly  
     65                70                75                80

gcg cag gtg gag ctc ttg ccc gac aga gac ccg gac agc gac ggg acc 288  
 Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Ser Asp Gly Thr  
                   85                  90                  95

aag atc agc aca gtg aaa gtc caa ggc aat gac atc tcc cac aag ctt	336
Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu	
100	105
105	110
cag att tcc aaa gtg agg aaa aag gat gaa ggc tta tat gag tgc agg	384
Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg	
115	120
120	125
gtg act gat gcc aac tac ggg gag ctt cag gaa cac aag gcc cag gcc	432
Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala	
130	135
135	140
tat ctg aaa gtc aat gcc aac agc cat gcc cgc aga atg cag gcc ttc	480
Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe	
145	150
150	155
155	160
gaa gcc tcg ccc atg tgg ctg cag gat atg aag ccc cgc aag aac gtc	528
Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys Pro Arg Lys Asn Val	
165	170
170	175
tcc gca gcc atc ccc agc agc atc cat ggc tct gcc aac caa cga acg	576
Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser Ala Asn Gln Arg Thr	
180	185
185	190
cac tcc acc tcc agc cct caa gtg gta gcc aaa atc ccc aaa caa agt	624
His Ser Thr Ser Ser Pro Gln Val Val Ala Lys Ile Pro Lys Gln Ser	
195	200
200	205
cca caa tca ggt atg gaa acc cat ttc gag cct ttt att tta cca ctc	672
Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro Phe Ile Leu Pro Leu	
210	215
215	220
aca aac gct cca cag aaa ggt cag tcg tat aga gta gac aga ttt atg	720
Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg Val Asp Arg Phe Met	
225	230
230	235
235	240
aat ggt gat ttt taa	735
Asn Gly Asp Phe	

<210> 48  
<211> 660  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(657)

<400> 48  
caa gca aaa ttt acc gag ttt ccg cgg aac gtg acg gcg acc gag ggg      48  
Gln Ala Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly  
1                5                10                15  
cag aat gtg gag atg tcc tgc gcc ttc cag agc ggc tcc gcc tcg gtg      96  
Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val  
20                25                30

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tat ctg gag atc caa tgg tgg ttc ctg cg <sup>g</sup> ggg ccg gag gac ctg gat		144
Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp		
35	40	45
ccc ggg gcc gag ggg gcc ggc gcg cag gtg gag ctc ttg ccc gac aga		192
Pro Gly Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg		
50	55	60
gac ccg gac agc gac ggg acc aag atc agc aca gtg aaa gtc caa ggc		240
Asp Pro Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly		
65	70	75
aat gac atc tcc cac aag ctt cag att tcc aaa gtg agg aaa aag gat		288
Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp		
85	90	95
gaa ggc tta tat gag tgc agg gtg act gat gcc aac tac ggg gag ctt		336
Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu		
100	105	110
cag gaa cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat		384
Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His		
115	120	125
gcc cgc aga atg cag gcc ttc gaa gcc tcg ccc atg tgg ctg cag gat		432
Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp		
130	135	140
atg aag ccc cgc aag aac gtc tcc gca gcc atc ccc agc agc atc cat		480
Met Lys Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His		
145	150	155
160		
ggc tct gcc aac caa cga acg cac tcc acc tcc agc cct caa gtg gta		528
Gly Ser Ala Asn Gln Arg Thr His Ser Thr Ser Pro Gln Val Val		
165	170	175
gcc aaa atc ccc aaa caa agt cca caa tca ggt atg gaa acc cat ttc		576
Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe		
180	185	190
gag cct ttt att tta cca ctc aca aac gct cca cag aaa ggt cag tcg		624
Glu Pro Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser		
195	200	205
tat aga gta gac aga ttt atg aat ggt gat ttt taa		660
Tyr Arg Val Asp Arg Phe Met Asn Gly Asp Phe		
210	215	

<210> 49

<211> 219

<212> PRT

<213> Homo sapiens

<400> 49

Gln Ala Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly		
1	5	10
		15

Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val		
20	25	30

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Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp  
35 40 45

Pro Gly Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg  
50 55 60

Asp Pro Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly  
65 70 75 80

Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp  
85 90 95

Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu  
100 105 110

Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His  
115 120 125

Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp  
130 135 140

Met Lys Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His  
145 150 155 160

Gly Ser Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val  
165 170 175

Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe  
180 185 190

Glu Pro Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser  
195 200 205

Tyr Arg Val Asp Arg Phe Met Asn Gly Asp Phe  
210 215

<210> 50

<211> 3196

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (268)...(1020)

<400> 50

cacgcgtccg cagccagccg gcggcggaga cacttcacgg cgtggcaacc cgggtctgtg 60

ccttgaagcc tccggatcg agccagctcg gtccatccct cactagtcgc aatcccctgt 120

gtccaagcta ctcttgcta tgagcggcag catgcgtgca gtatcgcgcc ccaggctctg 180

agagcagcct gcggacacgc ttgccttatct gtcttttag gttttggggc tctgggctac 240

acggatgtgc cccactccct tggcatg atg ggg atc ttt ttg gcg tct gtt gga 294

Met Gly Ile Phe Leu Ala Ser Val Gly

ttt atg ttc ttt tcc gtg tta tat gta caa caa ggg ctt tct tct caa Phe Met Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln	342
10 15 20 25	
gca aaa ttt acc gag ttg ccg aga aat gtg act gct acc gaa ggg caa Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly Gln	390
30 35 40	
aat gtg gag atg tcc tgt gct ttc caa agc ggc tct gct tca gtg tac Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr	438
45 50 55	
ctg gag atc cag tgg tgg ttc ctt cgg ggg cca gag gac ctg gag caa Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu Gln	486
60 65 70	
ggc acg gag gct gca ggc tcg cag gtg gag ctc tta ccc gac aga gac Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg Asp	534
75 80 85	
ccg gac aac gat ggg acc aag att agt aca gtg aaa gtc caa ggc aat Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn	582
90 95 100 105	
gat atc tcc cac aag ctt cag ata tcc aaa gtg aga aaa aag gat gaa Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu	630
110 115 120	
ggt tta tac gag tgc agg gtg act gac gct aac tac ggg gag ctt cag Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln	678
125 130 135	
gaa cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat gct Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala	726
140 145 150	
cgg agg atg cag gcc ttt gaa gcc tca cct atg tgg ctg caa gac acg Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Thr	774
155 160 165	
aag cct cga aag aac gca tca tcg gtg gtt ccc agc agc gtc cac aac Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His Asn	822
170 175 180 185	
tct gcc aac caa cga atg cac tcc acc tcc agc cct caa gcg gta gcc Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val Ala	870
190 195 200	
aaa atc ccc aag caa agt cca caa tca gca aag agc aaa tcg cct gta Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro Val	918
205 210 215	
aaa tct acg gag cgg aca gca aag ttg acc cta tac tcc aag cac cat Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His His	966
220 225 230	
tct gca ccc ctg tac tct agt tat cta cac aag gag cat cag ctt ccg Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu Pro	1014
235 240 245	

gaa gca taagtgaaga cactgtcaca cgctttattt ataataatttt ctttggaaag 1070  
Glu Ala  
250

ttgctgatct tttatttcaa gagaattaat ggaaagagat aggacatttt ccaattacaa 1130  
gaccaattttt tttccctttta tttcaacaaa taaaacctgc atttcactga ctgctcagga 1190  
gttggcctga atgacatcgat tatactaaat atttccatgg attccaccaa tttcctaacg 1250  
aggcacacct aatcttcaag aagcaaacaa agatggaaaa cctaagaacc acaaactgtc 1310  
tcatacagca ccccagctga ggaacaaaac aaatagctaa atgctgacca tggcaaatca 1370  
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tacattgagt gtggatata tcaatgtattt ttaattcatt tggcaatttc tgtataggca 1610  
aacctggcaa attctgtaaa ttgcttatacg tatgtgtatc atgacttcaa ggttagatagg 1670  
ctatgatgct catgcaagct gacttttttc attctatata caaatatattt catgagcata 1730  
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gtcctctact tccttctgga aaaattttaa attgtgtatc tctctgataa atgaattttat 1910  
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gtttggggat cttgagttga gtctgaagaa tgcacacctg gttttgaca gagttccctca 2030  
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atggtaaattt tttccttgcc attttttttc tttcatttga ttcatttattt cattctaaatg 2750

aagaaaataa aggtttaatt atgatacttt attaacatac aaatgtattt tctttctaag 2810  
ttaaatatct gaaagttgt aaaaatgatg gtagagaaat attactcatt cggttcttt 2870  
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ggggggaaaa tcatgtatta tactttact caatgtctag gtaatggatt cagctaatt 2990  
tacagcaagc caaatgtgt accgtatcag taatgttcac catgcttgcataaaaaggc 3050  
atatgctagt ttggaaagaa tgctcattag attcattgt atcgtgtcca aaataataaa 3110  
gacctgttta tcactgtgaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3170  
aaaaaaaaaa aaaaaaqqgc qqccqc 3196

<210> 51

<211> 251

<212> PBT

<213> Mus musculus

<400> 51

Met Gly Ile Phe Leu Ala Ser Val Gly Phe Met Phe Phe Ser Val Leu  
1 5 10 15

Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Leu Pro  
                  20                 25                         30

Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys Ala  
                  35                        40                        45

Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp Phe  
50 55 60

Leu Arg Gly Pro Glu Asp Leu Glu Gln Gly Thr Glu Ala Ala Gly Ser  
65 70 75 80

Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Asn Asp Gly Thr Lys  
85 90 95

Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu Gln  
100 105 110

Thr Asp Ala Asn Tyr Glu Leu Gln Glu His Lys Ala Gln Ala Tyr  
130 135 140

Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gin Ala Phe Glu  
145 150 155 160

Ala Ser Pro Met Trp Leu Gin Asp Thr Lys Pro Arg Lys Asn Ala Ser  
165 170 175

Ser Val Val Pro Ser Ser Val His Asn Ser Ala Asn Gin Arg Met His  
180 185 190

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Ser Thr Ser Ser Pro Gln Ala Val Ala Lys Ile Pro Lys Gln Ser Pro  
 195 200 205

Gln Ser Ala Lys Ser Lys Ser Pro Val Lys Ser Thr Glu Arg Thr Ala  
 210 215 220

Lys Leu Thr Leu Tyr Ser Lys His His Ser Ala Pro Leu Tyr Ser Ser  
 225 230 235 240

Tyr Leu His Lys Glu His Gln Leu Pro Glu Ala  
 245 250

<210> 52  
<211> 756  
<212> DNA  
<213> *Mus musculus*

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<221> CDS  
<222> (1)..(753)

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<400> 52
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Met Gly Ile Phe Leu Ala Ser Val Gly Phe Met Phe Phe Ser Val Leu
1          5          10         15

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tat gta caa caa ggg ctt tct tct caa gca aaa ttt acc gag ttg ccg 96  
 Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Leu Pro  
 20 25 30

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aga aat gtg act gct acc gaa ggg caa aat gtg gag atg tcc tgt gct 144
Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys Ala
          35           40           45

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ttc caa agc ggc tct gct tca gtg tac ctg gag atc cag tgg tgg ttc 192  
 Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp Phe  
 50 55 60

ctt cg<sup>g</sup> gg<sup>g</sup> cc<sup>a</sup> ga<sup>c</sup> ga<sup>c</sup> ct<sup>t</sup> ga<sup>g</sup> ca<sup>a</sup> gg<sup>c</sup> ac<sup>g</sup> ga<sup>g</sup> g<sup>c</sup>t g<sup>c</sup>a gg<sup>c</sup> tc<sup>g</sup> 240  
 Leu Arg Gly Pro Glu Asp Leu Glu Gln Gly Thr Glu Ala Ala Gly Ser  
     65                70                75                80

cag gtg gag ctc tta ccc gac aga gac ccg gac aac gat ggg acc aag 288  
Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Asn Asp Gly Thr Lys  
85 90 95

att agt aca gtg aaa gtc caa ggc aat gat atc tcc cac aag ctt cag 336  
 Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu Gln  
           100              105              110

ata tcc aaa gtg aga aaa aag gat gaa ggt tta tac gag tgc agg gtg 384  
 Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg Val  
 115 120 125

act gac gct aac tac ggg gag ctt cag gaa cac aag gcc cag gcc tat 432  
Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala Tyr  
130 135 140

ctg aaa gtc aat gcc aac agc cat gct cgg agg atg cag gcc ttt gaa		480
Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe Glu		
145	150	155
160		
gcc tca cct atg tgg ctg caa gac acg aag cct cga aag aac gca tca		528
Ala Ser Pro Met Trp Leu Gln Asp Thr Lys Pro Arg Lys Asn Ala Ser		
165	170	175
tcg gtg gtt ccc agc agc gtc cac aac tct gcc aac caa cga atg cac		576
Ser Val Val Pro Ser Ser Val His Asn Ser Ala Asn Gln Arg Met His		
180	185	190
tcc acc tcc agc cct caa gcg gta gcc aaa atc ccc aag caa agt cca		624
Ser Thr Ser Ser Pro Gln Ala Val Ala Lys Ile Pro Lys Gln Ser Pro		
195	200	205
caa tca gca aag agc aaa tcg cct gta aaa tct acg gag cgg aca gca		672
Gln Ser Ala Lys Ser Lys Ser Pro Val Lys Ser Thr Glu Arg Thr Ala		
210	215	220
aag ttg acc cta tac tcc aag cac cat tct gca ccc ctg tac tct agt		720
Lys Leu Thr Leu Tyr Ser Lys His His Ser Ala Pro Leu Tyr Ser Ser		
225	230	235
240		
tat cta cac aag gag cat cag ctt ccg gaa gca taa		756
Tyr Leu His Lys Glu His Gln Leu Pro Glu Ala		
245	250	
<210> 53		
<211> 684		
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<213> Mus musculus		
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<221> CDS		
<222> (1)..(681)		
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Gln Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly		
1	5	10
15		
caa aat gtg gag atg tcc tgt gct ttc caa agc ggc tct gct tca gtg		96
Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val		
20	25	30
tac ctg gag atc cag tgg tgg ttc ctt ccg ggg cca gag gac ctg gag		144
Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu		
35	40	45
caa ggc acg gag gct gca ggc tcg cag gtg gag ctc tta ccc gac aga		192
Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg		
50	55	60
gac ccg gac aac gat ggg acc aag att agt aca gtg aaa gtc caa ggc		240
Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly		
65	70	75
80		

aat gat atc tcc cac aag ctt cag ata tcc aaa gtg aga aaa aag gat Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp	85	90	95	288
gaa ggt tta tac gag tgc agg gtg act gac gct aac tac ggg gag ctt Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu	100	105	110	336
cag gaa cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His	115	120	125	384
gct cgg agg atg cag gcc ttt gaa gcc tca cct atg tgg ctg caa gac Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp	130	135	140	432
acg aag cct cga aag aac gca tca tcg gtg gtt ccc agc agc gtc cac Thr Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His	145	150	155	480
aac tct gcc aac caa cga atg cac tcc acc tcc agc cct caa gcg gta Asn Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val	165	170	175	528
gcc aaa atc ccc aag caa agt cca caa tca gca aag agc aaa tcg cct Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro	180	185	190	576
gta aaa tct acg gag cgg aca gca aag ttg acc cta tac tcc aag cac Val Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His	195	200	205	624
cat tct gca ccc ctg tac tct agt tat cta cac aag gag cat cag ctt His Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu	210	215	220	672
ccg gaa gca taa Pro Glu Ala 225				684

<210> 54  
<211> 227  
<212> PRT  
<213> Mus musculus

<400> 54				
Gln Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly	1	5	10	15
Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val	20	25	30	
Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu	35	40	45	
Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg	50	55	60	

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Asp	Pro	Asp	Asn	Asp	Gly	Thr	Lys	Ile	Ser	Thr	Val	Lys	Val	Gln	Gly		
65					70					75				80			
Asn	Asp	Ile	Ser	His	Lys	Leu	Gln	Ile	Ser	Lys	Val	Arg	Lys	Lys	Asp		
					85					90				95			
Glu	Gly	Leu	Tyr	Glu	Cys	Arg	Val	Thr	Asp	Ala	Asn	Tyr	Gly	Glu	Leu		
					100					105				110			
Gln	Glu	His	Lys	Ala	Gln	Ala	Tyr	Leu	Lys	Val	Asn	Ala	Asn	Ser	His		
					115					120				125			
Ala	Arg	Arg	Met	Gln	Ala	Phe	Glu	Ala	Ser	Pro	Met	Trp	Leu	Gln	Asp		
					130					135				140			
Thr	Lys	Pro	Arg	Lys	Asn	Ala	Ser	Ser	Val	Val	Pro	Ser	Ser	Val	His		
					145					150				155		160	
Asn	Ser	Ala	Asn	Gln	Arg	Met	His	Ser	Thr	Ser	Ser	Pro	Gln	Ala	Val		
					165					170				175			
Ala	Lys	Ile	Pro	Lys	Gln	Ser	Pro	Gln	Ser	Ala	Lys	Ser	Lys	Ser	Pro		
					180					185				190			
Val	Lys	Ser	Thr	Glu	Arg	Thr	Ala	Lys	Leu	Thr	Leu	Tyr	Ser	Lys	His		
					195					200				205			
His	Ser	Ala	Pro	Leu	Tyr	Ser	Ser	Tyr	Leu	His	Lys	Glu	His	Gln	Leu		
					210					215				220			
Pro	Glu	Ala															
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<210>	55																
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<213>	Homo sapiens																
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Gly	Gln	Asn	Val	Glu	Met	Ser	Cys	Ala	Phe	Gln	Ser	Gly	Ser	Ala	Ser		
					1					5				10		15	
Val	Tyr	Leu	Glu	Ile	Gln	Trp	Trp	Phe	Leu	Arg	Gly	Pro	Glu	Asp	Leu		
														20	25	30	
Asp	Pro	Gly	Ala	Glu	Gly	Ala	Gly	Ala	Gln	Val	Glu	Leu	Leu	Pro	Asp		
														35	40	45	
Arg	Asp	Pro	Asp	Ser	Asp	Gly	Thr	Lys	Ile	Ser	Thr	Val	Lys	Val	Gln		
														50	55	60	
Gly	Asn	Asp	Ile	Ser	His	Lys	Leu	Gln	Ile	Ser	Lys	Val	Arg	Lys	Lys		
														65	70	75	80
Asp	Glu	Gly	Leu	Tyr	Glu	Cys	Arg	Val									
														85			

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<210> 56  
<211> 89  
<212> PRT  
<213> Mus musculus

<400> 56  
Gly Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser  
1 5 10 15  
Val Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu  
20 25 30  
Glu Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp  
35 40 45  
Arg Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln  
50 55 60  
Gly Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys  
65 70 75 80  
Asp Glu Gly Leu Tyr Glu Cys Arg Val  
85

<210> 57  
<211> 47  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
sequence

<400> 57  
Gly Gln Ser Val Thr Leu Thr Cys Met Val Ser Phe His Pro Pro Asp  
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Tyr Thr Ile Trp Trp Tyr Arg Asn Gly Gln Pro Ile Thr Leu Thr Ile  
20 25 30  
Asn Ser Trp Gln Tyr Glu Asp Ser Glu Thr Tyr Trp Cys Met Val  
35 40 45

<210> 58  
<211> 2852  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (160)..(2178)

<400> 58  
gtcgaccac gcgtccggag cccggggcgg gtggacgcgg actcgaacgc agttgcttcg 60  
ggaccaggaa cccccctcggg cccgaccgc caggaaagac tgaggccgcg gcctgccccg 120

- 65 -

ccggctccc tgcgcggccg ccgcctcccg ggacagaag atg tgc tcc agg gtc Met Cys Ser Arg Val	174		
1	5		
cct ctg ctg ctg ccg ctc ctg cta ctg gcc ctg ggg cct ggg gtg Pro Leu Leu Leu Pro Leu Leu Leu Ala Leu Gly Pro Gly Val	222		
10	15	20	
cag ggc tgc cca tcc ggc tgc cag tgc agc cag cca cag aca gtc ttc Gln Gly Cys Pro Ser Gly Cys Gln Cys Ser Gln Pro Gln Thr Val Phe	270		
25	30	35	
tgc act gcc cgc cag ggg acc acg gtg ccc cga gac gtg cca ccc gac Cys Thr Ala Arg Gln Gly Thr Thr Val Pro Arg Asp Val Pro Pro Asp	318		
40	45	50	
acg gtg ggg ctg tac gtc ttt gag aac ggc atc acc atg ctc gac gca Thr Val Gly Leu Tyr Val Phe Glu Asn Gly Ile Thr Met Leu Asp Ala	366		
55	60	65	
ggc agc ttt gcc ggc ctg ccg ggc ctg cag ctc ctg gac ctg tca cag Gly Ser Phe Ala Gly Leu Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln	414		
70	75	80	85
aac cag atc gcc agc ctg ccc agc ggg gtc ttc cag cca ctc gcc aac Asn Gln Ile Ala Ser Leu Pro Ser Gly Val Phe Gln Pro Leu Ala Asn	462		
90	95	100	
ctc agc aac ctg gac ctg acg gcc aac agg ctg cat gaa atc acc aat Leu Ser Asn Leu Asp Leu Thr Ala Asn Arg Leu His Glu Ile Thr Asn	510		
105	110	115	
gag acc ttc cgt ggc ctg cgg cgc ctc gag cgc ctc tac ctg ggc aag Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu Arg Leu Tyr Leu Gly Lys	558		
120	125	130	
aac cgc atc cgc cac atc cag cct ggt gcc ttc gac acg ctc gac cgc Asn Arg Ile Arg His Ile Gln Pro Gly Ala Phe Asp Thr Leu Asp Arg	606		
135	140	145	
ctc ctg gag ctc aag ctg cag gac aac gag ctg cgg gca ctg ccc ccg Leu Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu Arg Ala Leu Pro Pro	654		
150	155	160	165
ctg cgc ctg ccc cgc ctg ctg ctg gac ctc agc cac aac agc ctc Leu Arg Leu Pro Arg Leu Leu Leu Asp Leu Ser His Asn Ser Leu	702		
170	175	180	
ctg gcc ctg gag ccc ggc atc ctg gac act gcc aac gtg gag ggc ctg Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu Ala Leu	750		
185	190	195	
cgg ctg gct ggt ctg ggg ctg cag cag ctg gac gag ggg ctc ttc agc Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly Leu Phe Ser	798		
200	205	210	
cgc ttg cgc aac ctc cac gac ctg gat gtg tcc gac aac cag ctg gag Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp Asn Gln Leu Glu	846		
215	220	225	

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cga gtg cca cct gtg atc cga ggc ctc cg <sup>g</sup> ctg acg cgc ctg cg <sup>g</sup>	894
Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly Leu Thr Arg Leu Arg	
230 235 240 245	
ctg gcc ggc aac acc cgc att gcc cag ctg cg <sup>g</sup> ccc gag gac ctg gcc	942
Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu Arg Pro Glu Asp Leu Ala	
250 255 260	
ggc ctg gct gcc ctg cag gag ctg gat gtg agc aac cta agc ctg cag	990
Gly Leu Ala Ala Leu Gln Glu Leu Asp Val Ser Asn Leu Ser Leu Gln	
265 270 275	
gcc ctg cct ggc gac ctc tcg ggc ctc ttc ccc cgc ctg cg <sup>g</sup> ctg ctg	1038
Ala Leu Pro Gly Asp Leu Ser Gly Leu Phe Pro Arg Leu Arg Leu Leu	
280 285 290	
gca gct gcc cgc aac ccc ttc aac tgc gtg tgc ccc ctg agc tgg ttt	1086
Ala Ala Ala Arg Asn Pro Phe Asn Cys Val Cys Pro Leu Ser Trp Phe	
295 300 305	
ggc ccc tgg gtg cgc gag agc cac gtc aca ctg gcc agc cct gag gag	1134
Gly Pro Trp Val Arg Glu Ser His Val Thr Leu Ala Ser Pro Glu Glu	
310 315 320 325	
acg cgc tgc cac ttc ccg ccc aag aac gct ggc cg <sup>g</sup> ctg ctc ctg gag	1182
Thr Arg Cys His Phe Pro Pro Lys Asn Ala Gly Arg Leu Leu Glu	
330 335 340	
ctt gac tac gcc gac ttt ggc tgc cca gcc acc acc acc aca gcc aca	1230
Leu Asp Tyr Ala Asp Phe Gly Cys Pro Ala Thr Thr Thr Ala Thr	
345 350 355	
gtg ccc acc acg agg ccc gtg gtg cg <sup>g</sup> gag ccc aca gcc ttg tct tct	1278
Val Pro Thr Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser	
360 365 370	
agc ttg gct cct acc tgg ctt agc ccc aca gcg ccg gcc act gag gcc	1326
Ser Leu Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala	
375 380 385	
ccc agc ccg ccc tcc act gcc cca ccg act gta ggg cct gtc ccc cag	1374
Pro Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln	
390 395 400 405	
ccc cag gac tgc cca ccg tcc acc tgc ctc aat ggg ggc aca tgc cac	1422
Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys His	
410 415 420	
ctg ggg aca ccg cac cac ctg gc <sup>g</sup> tgc ttg tgc ccc gaa ggc tt <sup>g</sup> acg	1470
Leu Gly Thr Arg His His Leu Ala Cys Leu Cys Pro Glu Gly Phe Thr	
425 430 435	
ggc ctg tac tgt gag agc cag atg ggg cag ggg aca ccg ccc agc cct	1518
Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg Pro Ser Pro	
440 445 450	
aca cca gtc acg ccg agg cca cca ccg tcc ctg acc ctg ggc atc gag	1566
Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr Leu Gly Ile Glu	
455 460 465	

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ccg gtg agc ccc acc tcc ctg cgc gtg ggg ctg cag cgc tac ctc cag		1614
Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu Gln Arg Tyr Leu Gln		
470	475	485
ggg agc tcc gtg cag ctc agg agc ctc cgt ctc acc tat cgc aac cta		1662
Gly Ser Ser Val Gln Leu Arg Ser Leu Arg Leu Thr Tyr Arg Asn Leu		
490	495	500
tcg ggc cct gat aag cgg ctg gtg acg ctg cga ctg cct gcc tcg ctc		1710
Ser Gly Pro Asp Lys Arg Leu Val Thr Leu Arg Leu Pro Ala Ser Leu		
505	510	515
gct gag tac acg gtc acc cag ctg cgg ccc aac gcc act tac tcc gtc		1758
Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro Asn Ala Thr Tyr Ser Val		
520	525	530
tgt gtc atg cct ttg ggg ccc ggg cgg gtg ccg gag ggc gag gag gcc		1806
Cys Val Met Pro Leu Gly Pro Gly Arg Val Pro Glu Gly Glu Glu Ala		
535	540	545
tgc ggg gag gcc cat aca ccc cca gcc gtc cac tcc aac cac gcc cca		1854
Cys Gly Glu Ala His Thr Pro Pro Ala Val His Ser Asn His Ala Pro		
550	555	560
565		
tgc acc cag gcc cgc gag ggc aac ctg ccg ctc ctc att gcg ccc gcc		1902
Val Thr Gln Ala Arg Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala		
570	575	580
ctg gcc gcg gtg ctc ctg gcc gcg ctg gct gcg gtg ggg gca gcc tac		1950
Leu Ala Ala Val Leu Ala Ala Leu Ala Val Gly Ala Ala Tyr		
585	590	595
tgt gtg cgg cgg ggg cgg gcc atg gca gca gcg gct cag gac aaa ggg		1998
Cys Val Arg Arg Gly Arg Ala Met Ala Ala Ala Gln Asp Lys Gly		
600	605	610
cag gtg ggg cca ggg gct ggg ccc ctg gaa ctg gag gga gtg aag gtc		2046
Gln Val Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val		
615	620	625
ccc ttg gag cca ggc ccg aag gca aca gag ggc ggt gga gag gcc ctg		2094
Pro Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Glu Ala Leu		
630	635	640
645		
ccc agc ggg tct gag tgt gag gtg cca ctc atg ggc ttc cca ggg cct		2142
Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly Pro		
650	655	660
ggc ctc cag tca ccc ctc cac gca aag ccc tac atc taagccagag		2188
Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr Ile		
665	670	
agagacaggg cagctggggc cgggtctca gccagtgaga tggccagccc cctcctgctg		2248
ccacaccacg taagttctca gtcccaacct cggggatgtg tgcagacagg gctgtgtgac		2308
cacagctggg ccctgttccc tctggacctc ggtctcctca tctgtgagat gctgtggccc		2368
agctgacgag ccctaacgtc cccagaaccg agtgcctatg aggacagtgt ccgccctgcc		2428

ctccgcaacg tgcagtcctt gggcacggcg ggccctgcca tgtgctggta acgcatgcct 2488  
 gggccctgtc gggctctccc actccaggcg gaccctgggg gccagtgaag gaagctcccg 2548  
 gaaagagcag agggagagcg ggtaggcggc tgtgtgactc tagtcttgc cccaggaagc 2608  
 gaaggaacaa aagaaactgg aaaggaagat gctttaggaa catgtttgc tttttaaaa 2668  
 tatatatata tttataagag atcccttccc atttattctg ggaagatgtt tttcaaactc 2728  
 agagacaagg actttggttt ttgtaagaca aacgatgata tgaaggcctt ttgtaagaaa 2788  
 aaataaaaaga tgaagtgtga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaggcg 2848  
 ccgc 2852

<210> 59  
 <211> 673  
 <212> PRT  
 <213> Homo sapiens

<400> 59  
 Met Cys Ser Arg Val Pro Leu Leu Leu Pro Leu Leu Leu Leu Ala  
 1 5 10 15  
 Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Ser Gln  
 20 25 30  
 Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro Arg  
 35 40 45  
 Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe Glu Asn Gly Ile  
 50 55 60  
 Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu Pro Gly Leu Gln Leu  
 65 70 75 80  
 Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser Leu Pro Ser Gly Val Phe  
 85 90 95  
 Gln Pro Leu Ala Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Arg Leu  
 100 105 110  
 His Glu Ile Thr Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu Arg  
 115 120 125  
 Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile Gln Pro Gly Ala Phe  
 130 135 140  
 Asp Thr Leu Asp Arg Leu Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu  
 145 150 155 160  
 Arg Ala Leu Pro Pro Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu  
 165 170 175  
 Ser His Asn Ser Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala  
 180 185 190

Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp  
 195 200 205  
 Glu Gly Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser  
 210 215 220  
 Asp Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly  
 225 230 235 240  
 Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu Arg  
 245 250 255  
 Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp Val Ser  
 260 265 270  
 Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly Leu Phe Pro  
 275 280 285  
 Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe Asn Cys Val Cys  
 290 295 300  
 Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Ser His Val Thr Leu  
 305 310 315 320  
 Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala Gly  
 325 330 335  
 Arg Leu Leu Leu Glu Leu Asp Tyr Ala Asp Phe Gly Cys Pro Ala Thr  
 340 345 350  
 Thr Thr Thr Ala Thr Val Pro Thr Thr Arg Pro Val Val Arg Glu Pro  
 355 360 365  
 Thr Ala Leu Ser Ser Ser Leu Ala Pro Thr Trp Leu Ser Pro Thr Ala  
 370 375 380  
 Pro Ala Thr Glu Ala Pro Ser Pro Pro Ser Thr Ala Pro Pro Thr Val  
 385 390 395 400  
 Gly Pro Val Pro Gln Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn  
 405 410 415  
 Gly Gly Thr Cys His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys  
 420 425 430  
 Pro Glu Gly Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly  
 435 440 445  
 Thr Arg Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu  
 450 455 460  
 Thr Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu  
 465 470 475 480  
 Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg Leu  
 485 490 495  
 Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr Leu Arg  
 500 505 510

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Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro Asn  
 515 520 525

Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro Gly Arg Val Pro  
 530 535 540

Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr Pro Pro Ala Val His  
 545 550 555 560

Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu Gly Asn Leu Pro Leu  
 565 570 575

Leu Ile Ala Pro Ala Leu Ala Ala Val Leu Leu Ala Ala Leu Ala Ala  
 580 585 590

Val Gly Ala Ala Tyr Cys Val Arg Arg Gly Arg Ala Met Ala Ala Ala  
 595 600 605

Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Ala Gly Pro Leu Glu Leu  
 610 615 620

Glu Gly Val Lys Val Pro Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly  
 625 630 635 640

Gly Gly Glu Ala Leu Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met  
 645 650 655

Gly Phe Pro Gly Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr  
 660 665 670

Ile

<210> 60

<211> 2019

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2019)

<400> 60

atg tgc tcc agg gtc cct ctg ctg ccg ctg ctc ctg cta ctg gcc	48
Met Cys Ser Arg Val Pro Leu Leu Pro Leu Leu Leu Leu Ala	
1 5 10 15	

ctg ggg cct ggg gtg cag ggc tgc cca tcc ggc tgc cag tgc agc cag	96
Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Ser Gln	
20 25 30	

cca cag aca gtc ttc tgc act gcc cgc cag ggg acc acg gtg ccc cga	144
Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro Arg	
35 40 45	

gac gtg cca ccc gac acg gtg ggg ctg tac gtc ttt gag aac ggc atc	192
Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe Glu Asn Gly Ile	
50 55 60	

acc atg ctc gac gca ggc agc ttt gcc ggc ctg ccg ggc ctg cag ctc		240	
Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu Pro Gly Leu Gln Leu			
65	70	75	80
ctg gac ctg tca cag aac cag atc gcc agc ctg ccc agc ggg gtc ttc		288	
Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser Leu Pro Ser Gly Val Phe			
85	90	95	
cag cca ctc gcc aac ctc agc aac ctg gac ctg acg gcc aac agg ctg		336	
Gln Pro Leu Ala Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Arg Leu			
100	105	110	
cat gaa atc acc aat gag acc ttc cgt ggc ctg cgg cgc ctc gag cgc		384	
His Glu Ile Thr Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu Arg			
115	120	125	
ctc tac ctg ggc aag aac cgc atc cgc cac atc cag cct ggt gcc ttc		432	
Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile Gln Pro Gly Ala Phe			
130	135	140	
gac acg ctc gac cgc ctc ctg gag ctc aag ctg cag gac aac gag ctg		480	
Asp Thr Leu Asp Arg Leu Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu			
145	150	155	160
cg <sub>g</sub> gca ctg ccc ccg ctg cgc ctg ccc cgc ctg ctg ctg ctg gac ctc		528	
Arg Ala Leu Pro Pro Leu Arg Leu Pro Arg Leu Leu Leu Asp Leu			
165	170	175	
agc cac aac agc ctc ctg gcc ctg gag ccc ggc atc ctg gac act gcc		576	
Ser His Asn Ser Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala			
180	185	190	
aac gtg gag gcg ctg cgg ctg gct ggt ctg ggg ctg cag cag ctg gac		624	
Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp			
195	200	205	
gag ggg ctc ttc agc cgc ttg cgc aac ctc cac gac ctg gat gtg tcc		672	
Glu Gly Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser			
210	215	220	
gac aac cag ctg gag cga gtg cca cct gtg atc cga ggc ctc cgg ggc		720	
Asp Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly			
225	230	235	240
ctg acg cgc ctg cgg ctg gcc ggc aac acc cgc att gcc cag ctg cgg		768	
Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu Arg			
245	250	255	
ccc gag gac ctg gcc ggc ctg gct gcc ctg cag gag ctg gat gtg agc		816	
Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp Val Ser			
260	265	270	
aac cta agc ctg cag gcc ctg cct ggc gac ctc tcg ggc ctc ttc ccc		864	
Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly Leu Phe Pro			
275	280	285	
cgc ctg cgg ctg ctg gca gct gcc cgc aac ccc ttc aac tgc gtg tgc		912	
Arg Leu Arg Leu Leu Ala Ala Arg Asn Pro Phe Asn Cys Val Cys			
290	295	300	

ccc ctg agc tgg ttt ggc ccc tgg gtg cgc gag agc cac gtc aca ctg		960	
Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Ser His Val Thr Leu			
305	310	315	320
gcc agc cct gag gag acg cgc tgc cac ttc ccg ccc aag aac gct ggc		1008	
Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala Gly			
325	330	335	
cgg ctg ctc ctg gag ctt gac tac gcc gac ttt ggc tgc cca gcc acc		1056	
Arg Leu Leu Leu Glu Leu Asp Tyr Ala Asp Phe Gly Cys Pro Ala Thr			
340	345	350	
acc acc aca gcc aca gtg ccc acc acg agg ccc gtg gtg cgg gag ccc		1104	
Thr Thr Ala Thr Val Pro Thr Thr Arg Pro Val Val Arg Glu Pro			
355	360	365	
aca gcc ttg tct tct agc ttg gct cct acc tgg ctt agc ccc aca gcg		1152	
Thr Ala Leu Ser Ser Leu Ala Pro Thr Trp Leu Ser Pro Thr Ala			
370	375	380	
ccg gcc act gag gcc ccc agc ccg ccc tcc act gcc cca ccg act gta		1200	
Pro Ala Thr Glu Ala Pro Ser Pro Ser Thr Ala Pro Pro Thr Val			
385	390	395	400
ggg cct gtc ccc cag ccc cag gac tgc cca ccg tcc acc tgc ctc aat		1248	
Gly Pro Val Pro Gln Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn			
405	410	415	
ggg ggc aca tgc cac ctg ggg aca cgg cac cac ctg gcg tgc ttg tgc		1296	
Gly Gly Thr Cys His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys			
420	425	430	
ccc gaa ggc ttc acg ggc ctg tac tgt gag agc cag atg ggg cag ggg		1344	
Pro Glu Gly Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly			
435	440	445	
aca cgg ccc agc cct aca cca gtc acg ccg agg cca cca ccg tcc ctg		1392	
Thr Arg Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu			
450	455	460	
acc ctg ggc atc gag ccg gtg agc ccc acc tcc ctg cgc gtg ggg ctg		1440	
Thr Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu			
465	470	475	480
cag cgc tac ctc cag ggg agc tcc gtg cag ctc agg agc ctc cgt ctc		1488	
Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg Leu			
485	490	495	
acc tat cgc aac cta tcg ggc cct gat aag cgg ctg gtg acg ctg cga		1536	
Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr Leu Arg			
500	505	510	
ctg cct gcc tcg ctc gct gag tac acg gtc acc cag ctg cgg ccc aac		1584	
Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro Asn			
515	520	525	
gcc act tac tcc gtc tgt gtc atg cct ttg ggg ccc ggg cgg gtg ccc		1632	
Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro Gly Arg Val Pro			
530	535	540	

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gag ggc gag gag gcc tgc ggg gag gcc cat aca ccc cca gcc gtc cac		1680
Glu Gly Glu Ala Cys Gly Glu Ala His Thr Pro Pro Ala Val His		
545	550	555
560		
tcc aac cac gcc cca gtc acc cag gcc cgc gag ggc aac ctg ccg ctc		1728
Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu Gly Asn Leu Pro Leu		
565	570	575
ctc att gcg ccc gcc ctg gcc gcg gtg ctc ctg gcc gcg ctg gct gcg		1776
Leu Ile Ala Pro Ala Leu Ala Val Leu Leu Ala Ala Leu Ala Ala		
580	585	590
gtg ggg gca gcc tac tgt gtg cgg cgg ggg cgg gcc atg gca gca gcg		1824
Val Gly Ala Ala Tyr Cys Val Arg Arg Gly Arg Ala Met Ala Ala Ala		
595	600	605
gct cag gac aaa ggg cag gtg ggg cca ggg gct ggg ccc ctg gaa ctg		1872
Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Ala Gly Pro Leu Glu Leu		
610	615	620
gag gga gtg aag gtc ccc ttg gag cca ggc ccg aag gca aca gag ggc		1920
Glu Gly Val Lys Val Pro Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly		
625	630	635
640		
ggt gga gag gcc ctg ccc agc ggg tct gag tgt gag gtg cca ctc atg		1968
Gly Gly Glu Ala Leu Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met		
645	650	655
ggc ttc cca ggg cct ggc ctc cag tca ccc ctc cac gca aag ccc tac		2016
Gly Phe Pro Gly Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr		
660	665	670
atc		2019
Ile		
<210> 61		
<211> 560		
<212> PRT		
<213> Homo sapiens		
<400> 61		
Met Leu Arg Gly Thr Leu Leu Cys Ala Val Leu Gly Leu Leu Arg Ala		
1	5	10
		15
Gln Pro Phe Pro Cys Pro Pro Ala Cys Lys Cys Val Phe Arg Asp Ala		
20	25	30
Ala Gln Cys Ser Gly Gly Asp Val Ala Arg Ile Ser Ala Leu Gly Leu		
35	40	45
Pro Thr Asn Leu Thr His Ile Leu Leu Phe Gly Met Gly Arg Gly Val		
50	55	60
Leu Gln Ser Gln Ser Phe Ser Gly Met Thr Val Leu Gln Arg Leu Met		
65	70	75
		80
Ile Ser Asp Ser His Ile Ser Ala Val Ala Pro Gly Thr Phe Ser Asp		
85	90	95

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Leu Ile Lys Leu Lys Thr Leu Arg Leu Ser Arg Asn Lys Ile Thr His  
100 105 110

Leu Pro Gly Ala Leu Leu Asp Lys Met Val Leu Leu Glu Gln Leu Phe  
115 120 125

Leu Asp His Asn Ala Leu Arg Gly Ile Asp Gln Asn Met Phe Gln Lys  
130 135 140

Leu Val Asn Leu Gln Glu Leu Ala Leu Asn Gln Asn Gln Leu Asp Phe  
145 150 155 160

Leu Pro Ala Ser Leu Phe Thr Asn Leu Glu Asn Leu Lys Leu Leu Asp  
165 170 175

Leu Ser Gly Asn Asn Leu Thr His Leu Pro Lys Gly Leu Leu Gly Ala  
180 185 190

Gln Ala Lys Leu Glu Arg Leu Leu His Ser Asn Arg Leu Val Ser  
195 200 205

Leu Asp Ser Gly Leu Leu Asn Ser Leu Gly Ala Leu Thr Glu Leu Gln  
210 215 220

Phe His Arg Asn His Ile Arg Ser Ile Ala Pro Gly Ala Phe Asp Arg  
225 230 235 240

Leu Pro Asn Leu Ser Ser Leu Thr Leu Ser Arg Asn His Leu Ala Phe  
245 250 255

Leu Pro Ser Ala Leu Phe Leu His Ser His Asn Leu Thr Leu Leu Thr  
260 265 270

Leu Phe Glu Asn Pro Leu Ala Glu Leu Pro Gly Val Leu Phe Gly Glu  
275 280 285

Met Gly Gly Leu Gln Glu Leu Trp Leu Asn Arg Thr Gln Leu Arg Thr  
290 295 300

Leu Pro Ala Ala Ala Phe Arg Asn Leu Ser Arg Leu Arg Tyr Leu Gly  
305 310 315 320

Val Thr Leu Ser Pro Arg Leu Ser Ala Leu Pro Gln Gly Ala Phe Gln  
325 330 335

Gly Leu Gly Glu Leu Gln Val Leu Ala Leu His Ser Asn Gly Leu Thr  
340 345 350

Ala Leu Pro Asp Gly Leu Leu Arg Gly Leu Gly Lys Leu Arg Gln Val  
355 360 365

Ser Leu Arg Arg Asn Arg Leu Arg Ala Leu Pro Arg Ala Leu Phe Arg  
370 375 380

Asn Leu Ser Ser Leu Glu Ser Val Gln Leu Asp His Asn Gln Leu Glu  
385 390 395 400

Thr Leu Pro Gly Asp Val Phe Gly Ala Leu Pro Arg Leu Thr Glu Val  
405 410 415

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Leu Leu Gly His Asn Ser Trp Arg Cys Asp Cys Gly Leu Gly Pro Phe  
 420 425 430

Leu Gly Trp Leu Arg Gln His Leu Gly Leu Val Gly Gly Glu Glu Pro  
 435 440 445

Pro Arg Cys Ala Gly Pro Gly Ala His Ala Gly Leu Pro Leu Trp Ala  
 450 455 460

Leu Pro Gly Gly Asp Ala Glu Cys Pro Gly Pro Arg Gly Pro Pro Pro  
 465 470 475 480

Arg Pro Ala Ala Asp Ser Ser Glu Ala Pro Val His Pro Ala Leu  
 485 490 495

Ala Pro Asn Ser Ser Glu Pro Trp Val Trp Ala Gln Pro Val Thr Thr  
 500 505 510

Gly Lys Gly Gln Asp His Ser Pro Phe Trp Gly Phe Tyr Phe Leu Leu  
 515 520 525

Leu Ala Val Gln Ala Met Ile Thr Val Ile Ile Val Phe Ala Met Ile  
 530 535 540

Lys Ile Gly Gln Leu Phe Arg Lys Leu Ile Arg Glu Arg Ala Leu Gly  
 545 550 555 560

<210> 62  
<211> 605  
<212> PRT  
<213> Papio hamadryas

<400> 62  
Met Ala Leu Arg Lys Gly Gly Leu Ala Leu Ala Leu Leu Leu Ser  
 1 5 10 15

Trp Val Ala Leu Gly Pro Arg Ser Leu Glu Gly Ala Glu Pro Gly Thr  
 20 25 30

Pro Gly Glu Ala Glu Gly Pro Ala Cys Pro Ala Thr Cys Ala Cys Ser  
 35 40 45

Tyr Asp Asp Glu Val Asn Glu Leu Ser Val Phe Cys Ser Ser Arg Asn  
 50 55 60

Leu Thr Arg Leu Pro Asp Gly Ile Pro Gly Gly Thr Gln Ala Leu Trp  
 65 70 75 80

Leu Asp Ser Asn Asn Leu Ser Ser Ile Pro Pro Ala Ala Phe Arg Asn  
 85 90 95

Leu Ser Ser Leu Ala Phe Leu Asn Leu Gln Gly Gly Gln Leu Gly Ser  
 100 105 110

Leu Glu Pro Gln Ala Leu Leu Gly Leu Glu Asn Leu Cys His Leu His  
 115 120 125

Leu Glu Arg Asn Gln Leu Arg Ser Leu Ala Val Gly Thr Phe Ala Tyr  
130 135 140

Thr Pro Ala Leu Ala Leu Leu Gly Leu Ser Asn Asn Arg Leu Ser Arg  
145 150 155 160

Leu Glu Asp Gly Leu Phe Glu Gly Leu Gly Asn Leu Trp Asp Leu Asn  
165 170 175

Leu Gly Trp Asn Ser Leu Ala Val Leu Pro Asp Ala Ala Phe Arg Gly  
180 185 190

Leu Gly Gly Leu Arg Glu Leu Val Leu Ala Gly Asn Arg Leu Ala Tyr  
195 200 205

Leu Gln Pro Ala Leu Phe Ser Gly Leu Ala Glu Leu Arg Glu Leu Asp  
210 215 220

Leu Ser Arg Asn Ala Leu Arg Ala Ile Lys Ala Asn Val Phe Ala Gln  
225 230 235 240

Leu Pro Arg Leu Gln Lys Leu Tyr Leu Asp Arg Asn Leu Ile Ala Ala  
245 250 255

Val Ala Pro Gly Ala Phe Leu Gly Leu Lys Ala Leu Arg Trp Leu Asp  
260 265 270

Leu Ser His Asn Arg Val Ala Gly Leu Leu Glu Asp Thr Phe Pro Gly  
275 280 285

Leu Leu Gly Leu Arg Val Leu Arg Leu Ser His Asn Ala Ile Ala Ser  
290 295 300

Leu Arg Pro Arg Thr Phe Glu Asp Leu His Phe Leu Glu Glu Leu Gln  
305 310 315 320

Leu Gly His Asn Arg Ile Arg Gln Leu Ala Glu Arg Ser Phe Glu Gly  
325 330 335

Leu Gly Gln Leu Glu Val Leu Thr Leu Asp His Asn Gln Leu Gln Glu  
340 345 350

Val Lys Val Gly Ala Phe Leu Gly Leu Thr Asn Val Ala Val Met Asn  
355 360 365

Leu Ser Gly Asn Cys Leu Arg Asn Leu Pro Glu Gln Val Phe Arg Gly  
370 375 380

Leu Gly Lys Leu His Ser Leu His Leu Glu Gly Ser Cys Leu Gly Arg  
385 390 395 400

Ile Arg Pro His Thr Phe Ala Gly Leu Ser Gly Leu Arg Arg Leu Phe  
405 410 415

Leu Lys Asp Asn Gly Leu Val Gly Ile Glu Glu Gln Ser Leu Trp Gly  
420 425 430

Leu Ala Glu Leu Leu Glu Leu Asp Leu Thr Ser Asn Gln Leu Thr His  
435 440 445

Leu Pro His Gln Leu Phe Gln Gly Leu Gly Lys Leu Glu Tyr Leu Leu  
450 455 460

Leu Ser His Asn Arg Leu Ala Glu Leu Pro Ala Asp Ala Leu Gly Pro  
465 470 475 480

Leu Gln Arg Ala Phe Trp Leu Asp Val Ser His Asn Arg Leu Glu Ala  
485 490 495

Leu Pro Gly Ser Leu Leu Ala Ser Leu Gly Arg Leu Arg Tyr Leu Asn  
500 505 510

Leu Arg Asn Asn Ser Leu Arg Thr Phe Thr Pro Gln Pro Pro Gly Leu  
515 520 525

Glu Arg Leu Trp Leu Glu Gly Asn Pro Trp Asp Cys Ser Cys Pro Leu  
530 535 540

Lys Ala Leu Arg Asp Phe Ala Leu Gln Asn Pro Ser Ala Val Pro Arg  
545 550 555 560

Phe Val Gln Ala Ile Cys Glu Gly Asp Asp Cys Gln Pro Pro Val Tyr  
565 570 575

Thr Tyr Asn Asn Ile Thr Cys Ala Ser Pro Pro Glu Val Ala Gly Leu  
580 585 590

Asp Leu Arg Asp Leu Gly Glu Ala His Phe Ala Pro Cys  
595 600 605

<210> 63

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Xaa at positions 1, 3-4, 6, 8-9, 11, 14, 15 may  
be any amino acid

<220>

<223> Xaa at positions 2, 5, 7, 13, 17 and 22 may be  
Leu, Ile, Val, Met, Ala, Phe or Tyr

<220>

<223> Xaa at position 10 may be Asn, Cys or Thr

<220>

<223> Xaa at positions 12, 16, 18-21, if present, may  
be any amino acid

<220>

<223> Description of Artificial Sequence: Consensus  
sequence

<400> 63

Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa  
20

<210> 64  
<211> 46  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Xaas at positions 2-7, 9-15, 17-28 and 32-45, if present, may be any amino acid

<220>  
<223> Xaa at position 30 may be any amino acid

<220>  
<223> Description of Artificial Sequence: Consensus sequence

<400> 64  
Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys  
1 5 10 15

Xaa Cys Xaa Cys Xaa  
20 25 30

Xaa Cys  
35 40 45

<210> 65  
<211> 38  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Xaas at positions 2-5, 7-11, 13-18, 24 and 26-33 may be any amino acid

<220>  
<223> Xaas at positions 19-22 and 24-37, if present, may be any amino acid

<220>  
<223> Description of Artificial Sequence: Consensus sequence

<400> 65  
Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Cys  
35

<210> 66  
<211> 73  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Consensus sequence

<400> 66  
Pro Ser Pro Pro Arg Asn Leu Arg Val Thr Asp Ile Thr Pro Thr Ser  
1 5 10 15

Ile Thr Val Ser Trp Thr Pro Pro Glu Gly Asn Gly Pro Ile Thr Gly  
20 25 30

Tyr Arg Ile Gln Tyr Arg Trp Pro Val Asn Asp Asn Glu Trp Asn Glu  
35 40 45

Phe Asn Val Pro Arg Thr Thr Asn Ser Tyr Thr Ile Thr Asn Leu Arg  
50 55 60

Pro Gly Thr Glu Tyr Glu Phe Arg Val  
65 70

<210> 67  
<211> 2815  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (197)..(2215)

<400> 67  
gtcgaccac gcgtccggga gccggagcca gagaccgggg ctggaaacc ccagccccggg 60  
acgggacgca gcagcctctg gatcccggga ccccgacact ctcaggacccg gccagagggtg 120  
aaggactgag gccccactga ggccttggac cgacccgcct ggctccttca gccgcagtgc 180  
tctcctggga cagaag atg cac tcc agg agc tgc ctg cca cct ctc ctg ttg 232  
Met His Ser Arg Ser Cys Leu Pro Pro Leu Leu Leu  
1 5 10

ttg ctt ctg gtg ctc ctg ggg tct gga gta cag ggt tgc cca tca ggc 280  
Leu Leu Leu Val Leu Leu Gly Ser Gly Val Gln Gly Cys Pro Ser Gly  
15 20 25

tgc cag tgc aac cag cca cag aca gtc ttc tgc act gcc cgt cag gga 328  
Cys Gln Cys Asn Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly  
30 35 40

acc aca gtg ccc cga gac gtg cca cct gac aca gtg ggc ctg tac atc 376  
Thr Thr Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Ile  
45 50 55 60

- 80 -

ttt gag aac ggc atc acg aca ctt gat gtg ggc tgt ttt gct ggc ctt		424
Phe Glu Asn Gly Ile Thr Thr Leu Asp Val Gly Cys Phe Ala Gly Leu		
65	70	75
ccg ggc ctg cag ctt ctg gac ttg tca cag aac cag atc act agc ctg		472
Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Thr Ser Leu		
80	85	90
ccc ggg ggc atc ttt cag cca ctt gtt aac ctc agt aac ctg gac ctg		520
Pro Gly Gly Ile Phe Gln Pro Leu Val Asn Leu Ser Asn Leu Asp Leu		
95	100	105
act gcc aac aaa ctg cac gag atc tcc aac gag acc ttc cgt ggc ctg		568
Thr Ala Asn Lys Leu His Glu Ile Ser Asn Glu Thr Phe Arg Gly Leu		
110	115	120
cg <sup>g</sup> cg <sup>c</sup> ctg gag cg <sup>c</sup> ctc tac ctg ggc aag aac cga att cg <sup>c</sup> cac atc		616
Arg Arg Leu Glu Arg Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile		
125	130	135
140		
caa ccg ggt gcc ttc gac gcg ctt gat cg <sup>c</sup> ctc ctg gag ctc aag ctg		664
Gln Pro Gly Ala Phe Asp Ala Leu Asp Arg Leu Leu Glu Leu Lys Leu		
145	150	155
cca gac aat gag ctt cgg gtg ttg ccc cca ttg cac ttg ccc cg <sup>c</sup> ctg		712
Pro Asp Asn Glu Leu Arg Val Leu Pro Pro Leu His Leu Pro Arg Leu		
160	165	170
ctg ctg ctt gac ctc agc cac aac agc atc cca gcc ctg gaa gcc gga		760
Leu Leu Leu Asp Leu Ser His Asn Ser Ile Pro Ala Leu Glu Ala Gly		
175	180	185
ata ctg gat acc gcc aat gta gag gca ttg agg ttg gct ggc cta ggg		808
Ile Leu Asp Thr Ala Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly		
190	195	200
ctg cgg cag ctg gat gag ggg ctt ttt ggc cg <sup>c</sup> ctt ctc aac ctc cat		856
Leu Arg Gln Leu Asp Glu Gly Leu Phe Gly Arg Leu Leu Asn Leu His		
205	210	215
220		
gac ttg gat gtt tct gac aac cag ttg gag cat atg cca tct gtg att		904
Asp Leu Asp Val Ser Asp Asn Gln Leu Glu His Met Pro Ser Val Ile		
225	230	235
caa ggc ctg cgt ggc ctg aca cg <sup>c</sup> ctg cgg ctg gct ggc aac acc cgt		952
Gln Gly Leu Arg Gly Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg		
240	245	250
att gcc cag ata cgg ccc gag gac ctc gct ggt ctg act gcc cta cag		1000
Ile Ala Gln Ile Arg Pro Glu Asp Leu Ala Gly Leu Thr Ala Leu Gln		
255	260	265
gaa ttg gat gtg agc aac cta agc ctg cag gcc ctg ccc agt gac ctc		1048
Glu Leu Asp Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Ser Asp Leu		
270	275	280
tcg agt ctc ttt ccc cg <sup>c</sup> ctg cg <sup>c</sup> ctc tta gca gct gcc agg aac ccc		1096
Ser Ser Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Arg Asn Pro		
285	290	295
300		

ttc aac tgc ttg tgc ccc ttg agc tgg ttt ggt cct tgg gtg cgt gag Phe Asn Cys Leu Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu 305	310	315	1144
aac cat gtt gtc ttg gcc agc cct gag gag acg cgt tgt cac ttt cca Asn His Val Val Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro 320	325	330	1192
ccc aag aat gct ggc cga ctg ctc ctg gat ctg gat tat gca gat ttt Pro Lys Asn Ala Gly Arg Leu Leu Leu Asp Leu Asp Tyr Ala Asp Phe 335	340	345	1240
ggc tgc cca gtc acc act acc acg gcc aca gta cct act ata agg tct Gly Cys Pro Val Thr Thr Ala Thr Val Pro Thr Ile Arg Ser 350	355	360	1288
act atc agg gaa ccc aca ctt tca act tct agc caa gct ccc acc tgg Thr Ile Arg Glu Pro Thr Leu Ser Thr Ser Gln Ala Pro Thr Trp 365	370	375	1336
ccc agc ctc aca gag cca act acc cag gcc tcc acc gta cta tcg act Pro Ser Leu Thr Glu Pro Thr Thr Gln Ala Ser Thr Val Leu Ser Thr 385	390	395	1384
gcc cca cca acc atg agg cca gct cct cag ccc cag gac tgt cca gca Ala Pro Pro Thr Met Arg Pro Ala Pro Gln Pro Gln Asp Cys Pro Ala 400	405	410	1432
tcc atc tgc ctg aat ggt ggt agc tgc cgt ttg gga gca aga cac cac Ser Ile Cys Leu Asn Gly Gly Ser Cys Arg Leu Gly Ala Arg His His 415	420	425	1480
tgg gag tgc cta tgc cct gag ggc ttc att ggc ctg tac tgt gag agt Trp Glu Cys Leu Cys Pro Glu Gly Phe Ile Gly Leu Tyr Cys Glu Ser 430	435	440	1528
cca gtg gag caa ggg atg aag ccc agc tcc ata cca gac act cca agg Pro Val Glu Gln Gly Met Lys Pro Ser Ser Ile Pro Asp Thr Pro Arg 445	450	455	1576
ccc cct cca ctg ctg cct ctc agc att gag ccg gtg agc ccc acc tcc Pro Pro Pro Leu Leu Pro Leu Ser Ile Glu Pro Val Ser Pro Thr Ser 465	470	475	1624
ttg cgt gtg aag ctg cag cgc tac ttg cag ggt aac act gtg cag cta Leu Arg Val Lys Leu Gln Arg Tyr Leu Gln Gly Asn Thr Val Gln Leu 480	485	490	1672
cgg agc ctc cgg ctc acc tat cgc aac ctg tct ggc cct gac aaa cga Arg Ser Leu Arg Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg 495	500	505	1720
ctg gtg aca tta cgg ctg cct gct tca ctt gca gag tat aca gtc acc Leu Val Thr Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr 510	515	520	1768
cag ctg cga ccc aat gcc acc tat tct atc tgt gtc aca ccc ttg gga Gln Leu Arg Pro Asn Ala Thr Tyr Ser Ile Cys Val Thr Pro Leu Gly 525	530	535	1816

gct gga cgg aca cct gaa ggt gag gag gcc tgt ggg gag gcc aac act Ala Gly Arg Thr Pro Glu Gly Glu Ala Cys Gly Glu Ala Asn Thr 545	550	555	1864
tcc cag gca gtc cgc tct aac cat gcc cca gtt acc cag gcc cgt gag Ser Gln Ala Val Arg Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu 560	565	570	1912
ggc aac ctg cca ctc ctc att gcg cct gcc ctg gct gta ctt ctg Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val Leu Leu 575	580	585	1960
gct gtg tta gcc gct gca ggg gca gcc tac tgt gtg cgg cgg gca cgg Ala Val Leu Ala Ala Gly Ala Ala Tyr Cys Val Arg Arg Ala Arg 590	595	600	2008
gca act tct aca gct cag gac aaa ggg cag gtg ggg cca ggg act gga Ala Thr Ser Thr Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Thr Gly 605	610	615	2056
ccc ctg gaa cta gag ggg gtg aaa gcc cct ttg gag cca ggc tcc aag Pro Leu Glu Leu Glu Gly Val Lys Ala Pro Leu Glu Pro Gly Ser Lys 625	630	635	2104
gca aca gag gga ggt ggg gag gct ttg tca ggt ggt cct gaa tgt gag Ala Thr Glu Gly Gly Glu Ala Leu Ser Gly Pro Glu Cys Glu 640	645	650	2152
gtg cct ctt atg ggc tac cca ggg ccc agc ctt cag ggg gtc ctc cct Val Pro Leu Met Gly Tyr Pro Gly Pro Ser Leu Gln Gly Val Leu Pro 655	660	665	2200
gct aag cac tac att tagactggtg agaaagagca gccagggggt caggcttca Ala Lys His Tyr Ile 670			2255
gtcaccaccc tcctgctgcc acagaaggaa gttctcagta tacaccacag tgcacgtgca tgatggagct gtgggaccct ctctgggctg ggtctcatct gtaagctgct acagccca tgaactctgc cagccgcccag tgcattccagt acagcgctg ccatcttgt caatgtcaa ccctggatg tgagccctgc catgtgctgg taacatggct aggcatgtt ggctccaa accatggagt ctggtaacca gtgaaggaag cccccagaaa taatgagtgg ggaaggtact agggcactgg ccttggcctc aaaagtgcag gcacacttga aactggaaag gaaggtgctc tggcacatg tggatttgct tctattgttt tggattgttt tttctaattgt attataaaa gatctttcc catttatgct gggaaagtgt tttcaaaact cagtgacaag gactttgg tttgcataagac tggatgtat atgaaggcct tttgcataagaa aataaaaaat aaagtaaaaa aaaaaaaaaa gggcgccgc			2815

<210> 68  
<211> 673  
<212> PRT  
<213> Mus musculus

<400> 68  
Met His Ser Arg Ser Cys Leu Pro Pro Leu Leu Leu Leu Leu Val  
1 5 10 15  
  
Leu Leu Gly Ser Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Asn  
20 25 30  
  
Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro  
35 40 45  
  
Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Ile Phe Glu Asn Gly  
50 55 60  
  
Ile Thr Thr Leu Asp Val Gly Cys Phe Ala Gly Leu Pro Gly Leu Gln  
65 70 75 80  
  
Leu Leu Asp Leu Ser Gln Asn Gln Ile Thr Ser Leu Pro Gly Gly Ile  
85 90 95  
  
Phe Gln Pro Leu Val Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Lys  
100 105 110  
  
Leu His Glu Ile Ser Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu  
115 120 125  
  
Arg Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile Gln Pro Gly Ala  
130 135 140  
  
Phe Asp Ala Leu Asp Arg Leu Leu Glu Leu Lys Leu Pro Asp Asn Glu  
145 150 155 160  
  
Leu Arg Val Leu Pro Pro Leu His Leu Pro Arg Leu Leu Leu Leu Asp  
165 170 175  
  
Leu Ser His Asn Ser Ile Pro Ala Leu Glu Ala Gly Ile Leu Asp Thr  
180 185 190  
  
Ala Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Arg Gln Leu  
195 200 205  
  
Asp Glu Gly Leu Phe Gly Arg Leu Leu Asn Leu His Asp Leu Asp Val  
210 215 220  
  
Ser Asp Asn Gln Leu Glu His Met Pro Ser Val Ile Gln Gly Leu Arg  
225 230 235 240  
  
Gly Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Ile  
245 250 255  
  
Arg Pro Glu Asp Leu Ala Gly Leu Thr Ala Leu Gln Glu Leu Asp Val  
260 265 270  
  
Ser Asn Leu Ser Leu Gln Ala Leu Pro Ser Asp Leu Ser Ser Leu Phe  
275 280 285

- 84 -

Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe Asn Cys Leu  
290 295 300

Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Asn His Val Val  
305 310 315 320

Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala  
325 330 335

Gly Arg Leu Leu Leu Asp Leu Asp Tyr Ala Asp Phe Gly Cys Pro Val  
340 345 350

Thr Thr Thr Ala Thr Val Pro Thr Ile Arg Ser Thr Ile Arg Glu  
355 360 365

Pro Thr Leu Ser Thr Ser Ser Gln Ala Pro Thr Trp Pro Ser Leu Thr  
370 375 380

Glu Pro Thr Thr Gln Ala Ser Thr Val Leu Ser Thr Ala Pro Pro Thr  
385 390 395 400

Met Arg Pro Ala Pro Gln Pro Gln Asp Cys Pro Ala Ser Ile Cys Leu  
405 410 415

Asn Gly Gly Ser Cys Arg Leu Gly Ala Arg His His Trp Glu Cys Leu  
420 425 430

Cys Pro Glu Gly Phe Ile Gly Leu Tyr Cys Glu Ser Pro Val Glu Gln  
435 440 445

Gly Met Lys Pro Ser Ser Ile Pro Asp Thr Pro Arg Pro Pro Pro Leu  
450 455 460

Leu Pro Leu Ser Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Lys  
465 470 475 480

Leu Gln Arg Tyr Leu Gln Gly Asn Thr Val Gln Leu Arg Ser Leu Arg  
485 490 495

Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr Leu  
500 505 510

Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro  
515 520 525

Asn Ala Thr Tyr Ser Ile Cys Val Thr Pro Leu Gly Ala Gly Arg Thr  
530 535 540

Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala Asn Thr Ser Gln Ala Val  
545 550 555 560

Arg Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu Gly Asn Leu Pro  
565 570 575

Leu Leu Ile Ala Pro Ala Leu Ala Ala Val Leu Leu Ala Val Leu Ala  
580 585 590

Ala Ala Gly Ala Ala Tyr Cys Val Arg Arg Ala Arg Ala Thr Ser Thr  
595 600 605

Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Thr Gly Pro Leu Glu Leu  
 610 615 620

Glu Gly Val Lys Ala Pro Leu Glu Pro Gly Ser Lys Ala Thr Glu Gly  
 625 630 635 640

Gly Gly Glu Ala Leu Ser Gly Gly Pro Glu Cys Glu Val Pro Leu Met  
 645 650 655

Gly Tyr Pro Gly Pro Ser Leu Gln Gly Val Leu Pro Ala Lys His Tyr  
 660 665 670

Ile

<210> 69  
<211> 2022  
<212> DNA  
<213> *Mus musculus*

<220>  
<221> CDS  
<222> (1)..(2019)

<400> 69  
atg cac tcc agg agc tgc ctg cca cct ctc ctg ttg ttg ctt ctg gtg 48  
Met His Ser Arg Ser Cys Leu Pro Pro Leu Leu Leu Leu Leu Leu Val  
1 5 10 15

ctc ctg ggg tct gga gta cag ggt tgc cca tca ggc tgc cag tgc aac 96  
 Leu Leu Gly Ser Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Asn  
                  20                 25                 30

cag cca cag aca gtc ttc tgc act gcc cgt cag gga acc aca gtg ccc 144  
 Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro  
           35                  40                  45

cga gac gtg cca cct gac aca gtg ggc ctg tac atc ttt gag aac ggc 192  
Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Ile Phe Glu Asn Gly  
50 55 60

atc acg aca ctt gat gtg ggc tgt ttt gct ggc ctt ccg ggc ctg cag 240  
 Ile Thr Thr Leu Asp Val Gly Cys Phe Ala Gly Leu Pro Gly Leu Gln  
 65 70 75 80

cct ctg gac ttg tca cag aac cag atc act agc ctg ccc ggg ggc atc 288  
Leu Leu Asp Leu Ser Gln Asn Gln Ile Thr Ser Leu Pro Gly Gly Ile  
85 90 95

ttt cag cca ctt gtt aac ctc agt aac ctg gac ctg act gcc aac aaa 336  
 Phe Gln Pro Leu Val Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Lys  
           100                 105                 110

ctg cac gag atc tcc aac gag acc ttc cgt ggc ctg cgg cgc ctg gag 384  
 Leu His Glu Ile Ser Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu  
 115 120 125

cgc ctc tac ctg ggc aag aac cga att	cgc cac atc caa ccg ggt gcc	432	
Arg Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile Gln Pro Gly Ala			
130	135	140	
ttc gac gcg ctt gat cgcc tcg gag ctc aag ctg cca gac aat gag		480	
Phe Asp Ala Leu Asp Arg Leu Leu Glu Leu Lys Leu Pro Asp Asn Glu			
145	150	155	160
ctt cgg gtg ttg ccc cca ttg cac ttg ccc cgc ctg ctg ctg ctt gac		528	
Leu Arg Val Leu Pro Pro Leu His Leu Pro Arg Leu Leu Leu Asp			
165	170	175	
ctc agc cac aac agc atc cca gcc ctg gaa gcc gga ata ctg gat acc		576	
Leu Ser His Asn Ser Ile Pro Ala Leu Glu Ala Gly Ile Leu Asp Thr			
180	185	190	
gcc aat gta gag gca ttg agg ttg gct ggc cta ggg ctg cgg cag ctg		624	
Ala Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Arg Gln Leu			
195	200	205	
gat gag ggg ctt ttt ggc cgc ctt ctc aac ctc cat gac ttg gat gtt		672	
Asp Glu Gly Leu Phe Gly Arg Leu Leu Asn Leu His Asp Leu Asp Val			
210	215	220	
tct gac aac cag ttg gag cat atg cca tct gtg att caa ggc ctg cgt		720	
Ser Asp Asn Gln Leu Glu His Met Pro Ser Val Ile Gln Gly Leu Arg			
225	230	235	240
ggc ctg aca cgc ctg cgg ctg gct ggc aac acc cgt att gcc cag ata		768	
Gly Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Ile			
245	250	255	
cgg ccc gag gac ctc gct ggt ctg act gcc cta cag gaa ttg gat gtg		816	
Arg Pro Glu Asp Leu Ala Gly Leu Thr Ala Leu Gln Glu Leu Asp Val			
260	265	270	
agc aac cta agc ctg cag gcc ctg ccc agt gac ctc tcg agt ctc ttt		864	
Ser Asn Leu Ser Leu Gln Ala Leu Pro Ser Asp Leu Ser Ser Leu Phe			
275	280	285	
ccc cgc ctg cgc ctc tta gca gct gcc agg aac ccc ttc aac tgc ttg		912	
Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe Asn Cys Leu			
290	295	300	
tgc ccc ttg agc tgg ttt ggt cct tgg gtg cgt gag aac cat gtt gtg		960	
Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Asn His Val Val			
305	310	315	320
ttg gcc agc cct gag gag acg cgt tgt cac ttt cca ccc aag aat gct		1008	
Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala			
325	330	335	
ggc cga ctg ctc ctg gat ctg gat tat gca gat ttt ggc tgc cca gtc		1056	
Gly Arg Leu Leu Leu Asp Leu Asp Tyr Ala Asp Phe Gly Cys Pro Val			
340	345	350	
acc act acc acg gcc aca gta cct act ata agg tct act atc agg gaa		1104	
Thr Thr Thr Ala Thr Val Pro Thr Ile Arg Ser Thr Ile Arg Glu			
355	360	365	

ccc aca ctt tca act tct agc caa gct ccc acc tgg ccc agc ctc aca		1152
Pro Thr Leu Ser Thr Ser Ser Gln Ala Pro Thr Trp Pro Ser Leu Thr		
370	375	380
gag cca act acc cag gcc tcc acc gta cta tcg act gcc cca cca acc		1200
Glu Pro Thr Thr Gln Ala Ser Thr Val Leu Ser Thr Ala Pro Pro Thr		
385	390	395
400		
atg agg cca gct cct cag ccc cag gac tgt cca gca tcc atc tgc ctg		1248
Met Arg Pro Ala Pro Gln Pro Asp Cys Pro Ala Ser Ile Cys Leu		
405	410	415
aat ggt ggt agc tgc cgt ttg gga gca aga cac cac tgg gag tgc cta		1296
Asn Gly Gly Ser Cys Arg Leu Gly Ala Arg His His Trp Glu Cys Leu		
420	425	430
tgc cct gag ggc ttc att ggc ctg tac tgt gag agt cca gtg gag caa		1344
Cys Pro Glu Gly Phe Ile Gly Leu Tyr Cys Glu Ser Pro Val Glu Gln		
435	440	445
ggg atg aag ccc agc tcc ata cca gac act cca agg ccc cct cca ctg		1392
Gly Met Lys Pro Ser Ser Ile Pro Asp Thr Pro Arg Pro Pro Pro Leu		
450	455	460
ctg cct ctc agc att gag ccg gtg agc ccc acc tcc ttg cgt gtg aag		1440
Leu Pro Leu Ser Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Lys		
465	470	475
480		
ctg cag cgc tac ttg cag ggt aac act gtg cag cta cggt agc ctc cgg		1488
Leu Gln Arg Tyr Leu Gln Gly Asn Thr Val Gln Leu Arg Ser Leu Arg		
485	490	495
ctc acc tat cgc aac ctg tct ggc cct gac aaa cga ctg gtg aca tta		1536
Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr Leu		
500	505	510
cgg ctg cct gct tca ctt gca gag tat aca gtc acc cag ctg cga ccc		1584
Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro		
515	520	525
aat gcc acc tat tct atc tgt gtc aca ccc ttg gga gct gga cgg aca		1632
Asn Ala Thr Tyr Ser Ile Cys Val Thr Pro Leu Gly Ala Gly Arg Thr		
530	535	540
cct gaa ggt gag gag gcc tgt ggg gag gcc aac act tcc cag gca gtc		1680
Pro Glu Gly Glu Ala Cys Gly Glu Ala Asn Thr Ser Gln Ala Val		
545	550	555
560		
cgc tct aac cat gcc cca gtt acc cag gcc cgt gag ggc aac ctg cca		1728
Arg Ser Asn His Ala Pro Val Thr Gin Ala Arg Glu Gly Asn Leu Pro		
565	570	575
ctc ctc att gcg cct gcc ctg gct gta ctt ctg gct gtg tta gcc		1776
Leu Leu Ile Ala Pro Ala Leu Ala Ala Val Leu Leu Ala Val Leu Ala		
580	585	590
595		
gct gca ggg gca gcc tac tgt gtg cggt cgg gca cgg gca act tct aca		1824
Ala Ala Gly Ala Ala Tyr Cys Val Arg Arg Ala Arg Ala Thr Ser Thr		
595	600	605

gct cag gac aaa ggg cag gtg ggg cca ggg act gga ccc ctg gaa cta	1872
Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Thr Gly Pro Leu Glu Leu	
610 615 620	
gag ggg gtg aaa gcc cct ttg gag cca ggc tcc aag gca aca gag gga	1920
Glu Gly Val Lys Ala Pro Leu Glu Pro Gly Ser Lys Ala Thr Glu Gly	
625 630 635 640	
ggt ggg gag gct ttg tca ggt ggt cct gaa tgt gag gtg cct ctt atg	1968
Gly Gly Glu Ala Leu Ser Gly Gly Pro Glu Cys Glu Val Pro Leu Met	
645 650 655	
ggc tac cca ggg ccc agc ctt cag ggg gtc ctc cct gct aag cac tac	2016
Gly Tyr Pro Gly Pro Ser Leu Gln Gly Val Leu Pro Ala Lys His Tyr	
660 665 670	
att tag	2022
Ile	

<210> 70	
<211> 2915	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (404)..(1294)	
<400> 70	
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agcgcggcgg cggcggcggc gcctaggaga gggagggcgc gcggggccga gcccacctag	120
cggagcgcgc cggccgcccc tggccgcgc cagcatgcgc cggccgcgg gccgctccgc	180
cggcagccac ccccgccggc ctcggcggcc tgcgctcggc cggggggcgc gggAACGCA	240
gccggagccg gaggcgggag cagcgagccg gagccccggg cgctcgaatg caggatgctc	300
gtggtccccca gcatccttga gccaccagga gtgagggctg ctgctccctg agacctggct	360
ccaaggagga tgccacagcc gcctgccagc tccggtctgc acc atg agt gat gag	415
Met Ser Asp Glu	
1	
cgg cgg ctg cct ggc agt gca gtg ggc tgg ctg gta tgt ggg ggc ctc	463
Arg Arg Leu Pro Gly Ser Ala Val Gly Trp Leu Val Cys Gly Gly Leu	
5 10 15 20	
tcc ctg ctg gcc aat gcc tgg ggc atc ctc agc gtt ggc gcc aag cag	511
Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val Gly Ala Lys Gln	
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Val Phe Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala Thr Cys Phe Ser		
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Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val Cys Trp Pro Val		
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Asn Tyr Arg Leu Ser Asn Ala Lys Lys Gln Ala Val His Thr Val Met		
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Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu Pro Ala Val Gly		
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Val Leu Asp Ser Thr Pro Ile Pro Glu Arg Ser Ala Val Arg Gln Gly		
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Glu Asp Trp Gly Lys Asp Gln Pro Glu Gly Phe His Pro Ser Ser Arg		
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Gln Asp Cys Leu Pro  
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Ile Ala Leu Phe Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala Asp  
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His Arg Ala Phe Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln Gly  
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Lys Arg Arg Ser Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser Leu  
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His Thr Val Met Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu  
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Leu	Cys	Val	Leu	Trp	Cys	Ser	Val	Ala	Gln	Ala	Leu	Leu	Leu	Pro	Val	
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Thr	Arg	Arg	Phe	Ser	His	Asp	Asp	Ala	Asp	Val	Trp	Ala	Ala	Val	Pro	
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gagttgtctt catagcacac ccagagccag ggatcccttt gtagttttt gacaacggag 4100  
catttctctt ctgtacagga cccaataaaa acttccttat gaaaaaaaaaaaaaggc 4160  
qqccqc 4166

<210> 74

<211> 609

<212> PRT

<213> Homo sapiens

<400> 74

Met Ser Asp Glu Arg Arg Leu Pro Gly Ser Ala Val Gly Trp Leu Val

1

5

10

15

Cys Gly Gly Leu Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val  
                   20                  25                  30

20

30

20

25

30

Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr  
50 55 60

50

55

60

Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu  
                   65                   70                   75                   80

65

70

75



- 99 -

Asp Val Trp Ala Ala Val Pro Leu Pro Ala Phe Leu Pro Arg Trp Gly  
 405 410 415

Ser Gly Glu Asp Leu Ala Ala Leu Ala His Leu Val Leu Pro Ala Gly  
 420 425 430

Pro Glu Arg Arg Ala Ser Leu Leu Ala Phe Ala Glu Asp Ala Pro  
 435 440 445

Pro Ser Arg Ala Arg Arg Ser Ala Glu Ser Leu Leu Ser Leu Arg  
 450 455 460

Thr Ser Ala Leu Asp Ser Gly Pro Arg Gly Ala Arg Asp Ser Pro Pro  
 465 470 475 480

Gly Ser Pro Arg Arg Pro Gly Pro Gly Pro Arg Ser Ala Ser Ala  
 485 490 495

Ser Leu Leu Pro Asp Ala Phe Ala Leu Thr Ala Phe Glu Cys Glu Pro  
 500 505 510

Gln Ala Leu Arg Arg Pro Pro Gly Pro Phe Pro Ala Ala Pro Ala Ala  
 515 520 525

Pro Asp Gly Ala Asp Pro Gly Glu Ala Pro Thr Pro Pro Ser Ser Ala  
 530 535 540

Gln Arg Ser Pro Gly Pro Arg Pro Ser Ala His Ser His Ala Gly Ser  
 545 550 555 560

Leu Arg Pro Gly Leu Ser Ala Ser Trp Gly Glu Pro Gly Gly Leu Arg  
 565 570 575

Ala Ala Gly Gly Gly Ser Thr Ser Ser Phe Leu Ser Ser Pro Ser  
 580 585 590

Glu Ser Ser Gly Tyr Ala Thr Leu His Ser Asp Ser Leu Gly Ser Ala  
 595 600 605

Ser

<210> 75  
 <211> 1827  
 <212> DNA  
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<220>  
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<400> 75  
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 Met Ser Asp Glu Arg Arg Leu Pro Gly Ser Ala Val Gly Trp Leu Val  
 1 5 10 15

tgt ggg ggc ctc tcc ctg ctg gcc aat gcc tgg ggc atc ctc agc gtt 96  
 Cys Gly Gly Leu Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val  
 20 25 30

- 100 -

ggc gcc aag cag aag aag tgg aag ccc ttg gag ttc ctg ctg tgt acg		144	
Gly Ala Lys Gln Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr			
35	40	45	
ctc gcg gcc acc cac atg cta aat gtg gcc gtg ccc atc gcc acc tac		192	
Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr			
50	55	60	
tcc gtg gtg cag ctg cgg cgg cag cgc ccc gac ttc gag tgg aat gag		240	
Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu			
65	70	75	80
ggt ctc tgc aag gtc ttc gtg tcc acc ttc tac acc ctc acc ctg gcc		288	
Gly Leu Cys Lys Val Phe Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala			
85	90	95	
acc tgt ttc tct gtc acc tcc ctc tac cac cgc atg tgg atg gtc		336	
Thr Cys Phe Ser Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val			
100	105	110	
tgc tgg cct gtc aac tac cgg ctg agc aat gcc aag aag cag gcg gtg		384	
Cys Trp Pro Val Asn Tyr Arg Leu Ser Asn Ala Lys Lys Gln Ala Val			
115	120	125	
cac aca gtc atg ggt atc tgg atg gtg tcc ttc atc ctg tcg gcc ctg		432	
His Thr Val Met Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu			
130	135	140	
cct gcc gtt ggc tgg cac gac acc agc gag cgc ttc tac acc cat ggc		480	
Pro Ala Val Gly Trp His Asp Thr Ser Glu Arg Phe Tyr Thr His Gly			
145	150	155	160
tgc cgc ttc atc gtg gct gag atc ggc ctg ggc ttt ggc gtc tgc ttc		528	
Cys Arg Phe Ile Val Ala Glu Ile Gly Leu Gly Phe Gly Val Cys Phe			
165	170	175	
ctg ctg ctg gtg ggc ggc agc gtg gcc atg ggc gtg atc tgc aca gcc		576	
Leu Leu Leu Val Gly Gly Ser Val Ala Met Gly Val Ile Cys Thr Ala			
180	185	190	
atc gcc ctc ttc cag acg ctg gcc gtg cag gtg ggg cgc cag gcc gac		624	
Ile Ala Leu Phe Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala Asp			
195	200	205	
cac cgc gcc ttc acc gtg ccc acc atc gtg gtg gag gac ggc cag ggc		672	
His Arg Ala Phe Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln Gly			
210	215	220	
aag cgg cgc tcc tcc atc gat ggc tcg gag ccc gcc aaa acc tct ctg		720	
Lys Arg Arg Ser Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser Leu			
225	230	235	240
cag acc acg ggc ctc gtg acc acc ata gtc ttc atc tac gac tgc ctc		768	
Gln Thr Thr Gly Leu Val Thr Ile Val Phe Ile Tyr Asp Cys Leu			
245	250	255	
atg ggc ttc cct gtg ctg gtg agc ttc agc agc ctg cgg gcc gac		816	
Met Gly Phe Pro Val Leu Val Val Ser Phe Ser Ser Leu Arg Ala Asp			
260	265	270	

gcc tca gcg ccc tgg atg gca ctc tgc gtg ctg tgg tgc tcc gtg gcc	864
Ala Ser Ala Pro Trp Met Ala Leu Cys Val Leu Trp Cys Ser Val Ala	
275 280 285	
cag gcc ctg ctg ctg cct gtg ttc ctc tgg gcc tgc gac cgc tac cgg	912
Gln Ala Leu Leu Pro Val Phe Leu Trp Ala Cys Asp Arg Tyr Arg	
290 295 300	
gct gac ctc aaa gct gtc cgg gag aag tgc atg gcc ctc atg gcc aac	960
Ala Asp Leu Lys Ala Val Arg Glu Lys Cys Met Ala Leu Met Ala Asn	
305 310 315 320	
gac gag gag tca gac gat gag acc agc ctg gaa ggt ggc atc tcc ccg	1008
Asp Glu Glu Ser Asp Asp Glu Thr Ser Leu Glu Gly Gly Ile Ser Pro	
325 330 335	
gac ctg gtg ttg gag cgc tcc ctg gac tat ggc tat gga ggt gat ttt	1056
Asp Leu Val Leu Glu Arg Ser Leu Asp Tyr Gly Tyr Gly Gly Asp Phe	
340 345 350	
gtg gcc cta gat agg atg gcc aag tat gag atc tcc gcc ctg gag ggg	1104
Val Ala Leu Asp Arg Met Ala Lys Tyr Glu Ile Ser Ala Leu Glu Gly	
355 360 365	
ggc ctg ccc cag ctc tac cca ctg cgg ccc ttg cag gag gac aag atg	1152
Gly Leu Pro Gln Leu Tyr Pro Leu Arg Pro Leu Gln Glu Asp Lys Met	
370 375 380	
caa tac ctg cag gtc ccg ccc acg cgg cgc ttc tcc cac gac gat gcg	1200
Gln Tyr Leu Gln Val Pro Pro Thr Arg Arg Phe Ser His Asp Asp Ala	
385 390 395 400	
gac gtg tgg gcc gcc gtc ccg ctg ccc gcc ttc ctg ccg cgc tgg ggc	1248
Asp Val Trp Ala Ala Val Pro Leu Pro Ala Phe Leu Pro Arg Trp Gly	
405 410 415	
tcc ggc gag gac ctg gcc ctg gcg cac ctg gtg ctg cct gcc ggg	1296
Ser Gly Glu Asp Leu Ala Ala Leu Ala His Leu Val Leu Pro Ala Gly	
420 425 430	
ccc gag cgg cgc cgc gcc agc ctc ctg gcc ttc gcg gag gac gca cca	1344
Pro Glu Arg Arg Ala Ser Leu Leu Ala Phe Ala Glu Asp Ala Pro	
435 440 445	
ccg tcc cgc ggc cgc cgc tcg gcc gag agc ctg ctg tcg ctg cgg	1392
Pro Ser Arg Ala Arg Arg Ser Ala Glu Ser Leu Leu Ser Leu Arg	
450 455 460	
acc tcg gcc ctg gat agc ggc ccg cgg gga gcc cgc gac tcg ccc ccc	1440
Thr Ser Ala Leu Asp Ser Gly Pro Arg Gly Ala Arg Asp Ser Pro Pro	
465 470 475 480	
ggc agc ccg cgc cgc cgc ccc ggg ccc ggc ccc cgc tcc gcc tcg gcc	1488
Gly Ser Pro Arg Arg Pro Gly Pro Gly Pro Arg Ser Ala Ser Ala	
485 490 495	
tcg ctg ctg ccc gac gcc ttc gcc ctg acc gcc ttc gag tgc gag cca	1536
Ser Leu Leu Pro Asp Ala Phe Ala Leu Thr Ala Phe Glu Cys Glu Pro	
500 505 510	

cag	gcc	ctg	cgc	cgc	ccg	ccc	ggg	ccc	ttc	ccc	gct	gcg	ccc	gcc	gcc	1584
Gln	Ala	Leu	Arg	Arg	Pro	Pro	Gly	Pro	Phe	Pro	Ala	Ala	Pro	Ala	Ala	
515									520						525	
ccc	gac	ggc	gca	gat	ccc	gga	gag	gcc	ccg	acg	ccc	cca	agc	agc	gcc	1632
Pro	Asp	Gly	Ala	Asp	Pro	Gly	Glu	Ala	Pro	Thr	Pro	Pro	Ser	Ser	Ala	
530									535						540	
cag	cgg	agc	cca	ggg	cca	cgc	ccc	tct	gct	cac	tcg	cac	gcc	ggc	tct	1680
Gln	Arg	Ser	Pro	Gly	Pro	Arg	Pro	Ser	Ala	His	Ser	His	Ala	Gly	Ser	
545									550						555	
ctg	cgc	ccc	ggc	ctg	agc	gct	tgg	ggc	gag	ccc	ggg	ggg	ctg	cgc	1728	
Leu	Arg	Pro	Gly	Leu	Ser	Ala	Ser	Trp	Gly	Glu	Pro	Gly	Gly	Leu	Arg	
									565						570	
gct	gct	ggc	ggc	ggc	ggc	ggc	ggc	acc	acc	agc	ttc	ctg	agt	tcc	ccc	1776
Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Ser	Thr	Ser	Ser	Phe	Leu	Ser	
									580						585	
gag	tcc	tcg	ggc	tac	gcc	acg	ctg	cac	tcg	gac	tcg	ctg	ggc	tcc	gct	1824
Glu	Ser	Ser	Gly	Tyr	Ala	Thr	Leu	His	Ser	Asp	Ser	Leu	Gly	Ser	Ala	
									595						600	
															605	
tcc																1827
Ser																
<210>	76															
<211>	177															
<212>	PRT															
<213>	Homo sapiens															
<220>																
<223>	Xaas at positions 38, 55 and 56 may be any amino acid															
<400>	76															
Gly	Asn	Ile	Leu	Val	Ile	Trp	Val	Ile	Cys	Arg	Tyr	Arg	Arg	Met	Arg	
1															15	
Thr	Pro	Met	Asn	Tyr	Phe	Ile	Val	Asn	Leu	Ala	Val	Ala	Asp	Leu	Leu	
20									25						30	
Phe	Ser	Leu	Phe	Thr	Xaa	Met	Pro	Phe	Trp	Met	Val	Tyr	Tyr	Val	Met	
35									40						45	
Gln	Gly	Arg	Trp	Pro	Phe	Xaa	Xaa	Gly	Asp	Phe	Met	Cys	Arg	Ile	Trp	
50									55						60	
Met	Tyr	Phe	Asp	Tyr	Met	Asn	Met	Tyr	Ala	Ser	Ile	Phe	Phe	Leu	Thr	
65									70						75	
Cys	Ile	Ser	Ile	Asp	Arg	Tyr	Leu	Trp	Ala	Ile	Cys	His	Pro	Met	Arg	
85										90					95	
Tyr	Met	Arg	Trp	Met	Thr	Pro	Arg	His	Arg	Ala	Trp	Val	Met	Ile	Ile	
100									105						110	

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Ile	Ile	Trp	Val	Met	Ser	Phe	Leu	Ile	Ser	Met	Pro	Pro	Phe	Leu	Met
115							120							125	

Phe	Arg	Trp	Ser	Thr	Tyr	Arg	Asp	Glu	Asn	Glu	Trp	Asn	Met	Thr	Trp
130							135						140		

Cys	Met	Ile	Tyr	Asp	Trp	Pro	Glu	Trp	Met	Trp	Arg	Trp	Tyr	Val	Ile
145							150					155			160

Leu	Met	Thr	Ile	Ile	Met	Gly	Phe	Tyr	Ile	Pro	Met	Ile	Ile	Met	Leu
									165		170			175	

Phe

<210> 77

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<223> Xaa at position 84 may be any amino acid

<400> 77

Ile	Gln	Glu	Arg	Met	Asn	Glu	Leu	Asn	Asp	Arg	Trp	Glu	Arg	Leu	Lys
1							5					10			15

Glu	Leu	Met	Glu	Gln	Arg	Arg	Gln	Met	Leu	Glu	Asp	Ser	Met	Arg	Leu
								20				25			30

Gln	Gln	Phe	Phe	Arg	Asp	Met	Asp	Glu	Glu	Glu	Ser	Trp	Ile	Asn	Glu
								35				40			45

Lys	Glu	Gln	Ile	Leu	Asn	Ser	Asp	Asp	Tyr	Gly	Lys	Asp	Leu	Thr	Ser
								50			55			60	

Val	Gln	Asn	Leu	Leu	Lys	Lys	His	Gln	Ala	Phe	Glu	Ala	Asp	Ile	Ala
								65			70			75	

Ala	His	Glu	Xaa	Asp	Arg	Ile	Gln	Ala	Leu	Asn	Glu	Phe	Ala	Gln	Gln
								85			90			95	

Leu	Ile	Gln	Glu	Asn	His	Tyr	Ala	Ser	Glu	Glu					
								100			105				

<210> 78

<211> 588

<212> PRT

<213> Homo sapiens

<400> 78

Met	Ala	Arg	Gly	Gly	Ala	Gly	Ala	Glu	Glu	Ala	Ser	Leu	Arg	Ser	Asn
1								5				10			15

Ala	Leu	Ser	Trp	Leu	Ala	Cys	Gly	Leu	Leu	Ala	Leu	Leu	Ala	Asn	Ala
								20				25			30

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Trp	Ile	Ile	Leu	Ser	Ile	Ser	Ala	Lys	Gln	Gln	Lys	His	Lys	Pro	Leu
35							40					45			
Glu	Leu	Leu	Leu	Cys	Phe	Leu	Ala	Gly	Thr	His	Ile	Leu	Met	Ala	Ala
50						55					60				
Val	Pro	Leu	Thr	Thr	Phe	Ala	Val	Val	Gln	Leu	Arg	Arg	Gln	Ala	Ser
65					70				75			80			
Ser	Asp	Tyr	Asp	Trp	Asn	Glu	Ser	Ile	Cys	Lys	Val	Phe	Val	Ser	Thr
					85				90			95			
Tyr	Tyr	Thr	Leu	Ala	Leu	Ala	Thr	Cys	Phe	Thr	Val	Ala	Ser	Leu	Ser
						100		105				110			
Tyr	His	Arg	Met	Trp	Met	Val	Arg	Trp	Pro	Val	Asn	Tyr	Arg	Leu	Ser
					115		120				125				
Asn	Ala	Lys	Lys	Gln	Ala	Leu	His	Ala	Val	Met	Gly	Ile	Trp	Met	Val
					130		135				140				
Ser	Phe	Ile	Leu	Ser	Thr	Leu	Pro	Ser	Ile	Gly	Trp	His	Asn	Asn	Gly
145						150			155			160			
Glu	Arg	Tyr	Tyr	Ala	Arg	Gly	Cys	Gln	Phe	Ile	Val	Ser	Lys	Ile	Gly
					165			170				175			
Leu	Gly	Phe	Gly	Val	Cys	Phe	Ser	Leu	Leu	Leu	Gly	Gly	Ile	Val	
					180			185				190			
Met	Gly	Leu	Val	Cys	Val	Ala	Ile	Thr	Phe	Tyr	Gln	Thr	Leu	Trp	Ala
					195			200			205				
Arg	Pro	Arg	Arg	Ala	Arg	Gln	Ala	Arg	Arg	Val	Gly	Gly	Gly	Gly	
					210		215				220				
Thr	Lys	Ala	Gly	Gly	Pro	Gly	Ala	Leu	Gly	Thr	Arg	Pro	Ala	Phe	Glu
					225		230			235			240		
Val	Pro	Ala	Ile	Val	Val	Glu	Asp	Ala	Arg	Gly	Lys	Arg	Arg	Ser	Ser
					245			250				255			
Leu	Asp	Gly	Ser	Glu	Ser	Ala	Lys	Thr	Ser	Leu	Gln	Val	Thr	Asn	Leu
					260			265				270			
Val	Ser	Ala	Ile	Val	Phe	Leu	Tyr	Asp	Ser	Leu	Thr	Gly	Val	Pro	Ile
					275			280			285				
Leu	Val	Val	Ser	Phe	Phe	Ser	Leu	Lys	Ser	Asp	Ser	Ala	Pro	Pro	Trp
					290		295				300				
Met	Val	Leu	Ala	Val	Leu	Trp	Cys	Ser	Met	Ala	Gln	Thr	Leu	Leu	
					305		310			315			320		
Pro	Ser	Phe	Ile	Trp	Ser	Cys	Glu	Arg	Tyr	Arg	Ala	Asp	Val	Arg	Thr
					325			330			335				
Val	Trp	Glu	Gln	Cys	Val	Ala	Ile	Met	Ser	Glu	Glu	Asp	Gly	Asp	Asp
					340			345			350				

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Asp	Gly	Gly	Cys	Asp	Asp	Tyr	Ala	Glu	Gly	Arg	Val	Cys	Lys	Val	Arg
355							360					365			
Phe	Asp	Ala	Asn	Gly	Ala	Thr	Gly	Pro	Gly	Ser	Arg	Asp	Pro	Ala	Gln
370						375					380				
Val	Lys	Leu	Leu	Pro	Gly	Arg	His	Met	Leu	Phe	Pro	Pro	Leu	Glu	Arg
385					390				395				400		
Val	His	Tyr	Leu	Gln	Val	Pro	Leu	Ser	Arg	Arg	Leu	Ser	His	Asp	Glu
					405			410					415		
Thr	Asn	Ile	Phe	Ser	Thr	Pro	Arg	Glu	Pro	Gly	Ser	Phe	Leu	His	Lys
					420			425					430		
Trp	Ser	Ser	Ser	Asp	Asp	Ile	Arg	Val	Leu	Pro	Ala	Gln	Ser	Arg	Ala
					435			440			445				
Leu	Gly	Gly	Pro	Pro	Glu	Tyr	Leu	Gly	Gln	Arg	His	Arg	Leu	Glu	Asp
					450			455			460				
Glu	Glu	Asp	Glu	Glu	Glu	Ala	Glu	Gly	Gly	Leu	Ala	Ser	Leu	Arg	
					465			470			475			480	
Gln	Phe	Leu	Glu	Ser	Gly	Val	Leu	Gly	Ser	Gly	Gly	Pro	Pro	Arg	
					485			490			495				
Gly	Pro	Gly	Phe	Phe	Arg	Glu	Glu	Ile	Thr	Thr	Phe	Ile	Asp	Glu	Thr
					500			505					510		
Pro	Leu	Pro	Ser	Pro	Thr	Ala	Ser	Pro	Gly	His	Ser	Pro	Arg	Arg	Pro
					515			520			525				
Arg	Pro	Leu	Gly	Leu	Ser	Pro	Arg	Arg	Leu	Ser	Leu	Gly	Ser	Pro	Glu
					530			535			540				
Ser	Arg	Ala	Val	Gly	Leu	Pro	Leu	Gly	Leu	Ser	Ala	Gly	Arg	Arg	Cys
					545			550			555			560	
Ser	Leu	Thr	Gly	Gly	Glu	Glu	Ser	Ala	Arg	Ala	Trp	Gly	Gly	Ser	Trp
					565			570			575				
Gly	Pro	Gly	Asn	Pro	Ile	Phe	Pro	Gln	Leu	Thr	Leu				
					580			585							

<210> 79

<211> 227

<212> PRT

<213> Homo sapiens

<400> 79

Ile	Thr	Phe	Tyr	Gln	Thr	Leu	Trp	Ala	Arg	Pro	Arg	Arg	Ala	Arg	Gln
1					5				10			15			

Ala	Arg	Arg	Val	Gly	Gly	Gly	Gly	Thr	Lys	Ala	Gly	Gly	Pro	Gly	
								25					30		

Ala	Leu	Gly	Thr	Arg	Pro	Ala	Phe	Glu	Val	Pro	Ala	Ile	Val	Val	Glu
						35		40			45				

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Asp	Ala	Arg	Gly	Lys	Arg	Arg	Ser	Ser	Leu	Asp	Gly	Ser	Glu	Ser	Ala
50					55						60				
Lys	Thr	Ser	Leu	Gln	Val	Thr	Asn	Leu	Val	Val	Ser	Phe	Phe	Ser	Leu
65					70					75					80
Lys	Ser	Asp	Ser	Ala	Pro	Pro	Trp	Met	Val	Leu	Ala	Val	Leu	Trp	Cys
					85				90					95	
Ser	Met	Ala	Gln	Thr	Leu	Leu	Leu	Pro	Ser	Phe	Ile	Trp	Ser	Cys	Glu
					100				105					110	
Arg	Tyr	Arg	Ala	Asp	Val	Arg	Thr	Val	Trp	Glu	Gln	Cys	Val	Ala	Ile
					115				120					125	
Met	Ser	Glu	Glu	Asp	Gly	Asp	Asp	Asp	Gly	Gly	Cys	Asp	Asp	Tyr	Ala
					130				135					140	
Glu	Gly	Arg	Val	Cys	Lys	Val	Arg	Phe	Asp	Ala	Asn	Gly	Ala	Thr	Gly
					145				150			155			160
Pro	Gly	Ser	Arg	Asp	Pro	Ala	Gln	Val	Lys	Leu	Leu	Pro	Gly	Arg	His
					165				170					175	
Met	Leu	Phe	Pro	Pro	Leu	Glu	Arg	Val	His	Tyr	Leu	Gln	Leu	Lys	Lys
					180				185					190	
Leu	Asp	Leu	Ala	Ala	Ala	Ala	Ala	His	Thr	Phe	Phe	Val	Ala	Asn	Pro
					195				200					205	
Met	His	Leu	Gln	Met	Arg	Glu	Asp	Met	Ala	Lys	Tyr	Arg	Arg	Met	Ser
					210				215					220	
Gly	Val	Arg													
		225													
<210>	80														
<211>	425														
<212>	PRT														
<213>	Homo sapiens														
<400>	80														
Met	Gly	Pro	Arg	Arg	Leu	Leu	Leu	Val	Ala	Ala	Cys	Phe	Ser	Leu	Cys
					1				5			10			15
Gly	Pro	Leu	Leu	Ser	Ala	Arg	Thr	Arg	Ala	Arg	Arg	Pro	Glu	Ser	Lys
					20				25					30	
Ala	Thr	Asn	Ala	Thr	Leu	Asp	Pro	Arg	Ser	Phe	Leu	Leu	Arg	Asn	Pro
					35				40					45	
Asn	Asp	Lys	Tyr	Glu	Pro	Phe	Trp	Glu	Asp	Glu	Glu	Lys	Asn	Glu	Ser
					50				55			60			
Gly	Leu	Thr	Glu	Tyr	Arg	Leu	Val	Ser	Ile	Asn	Lys	Ser	Ser	Pro	Leu
					65				70			75			80

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Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu  
 85 90 95  
 Thr Ser Ser Trp Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val  
 100 105 110  
 Phe Val Val Ser Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile  
 115 120 125  
 Leu Lys Met Lys Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu  
 130 135 140  
 Ala Thr Ala Asp Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser  
 145 150 155 160  
 Tyr Tyr Phe Ser Gly Ser Asp Trp Gln Phe Gly Ser Glu Leu Cys Arg  
 165 170 175  
 Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu Leu  
 180 185 190  
 Met Thr Val Ile Ser Ile Asp Arg Phe Leu Ala Val Val Tyr Pro Met  
 195 200 205  
 Gln Ser Leu Ser Trp Arg Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu  
 210 215 220  
 Ala Ile Trp Ala Leu Ala Ile Ala Gly Val Val Pro Leu Val Leu Lys  
 225 230 235 240  
 Glu Gln Thr Ile Gln Val Pro Gly Leu Asn Ile Thr Thr Cys His Asp  
 245 250 255  
 Val Leu Asn Glu Thr Leu Leu Glu Gly Tyr Tyr Ala Tyr Tyr Phe Ser  
 260 265 270  
 Ala Phe Ser Ala Val Phe Phe Val Pro Leu Ile Ile Ser Thr Val  
 275 280 285  
 Cys Tyr Val Ser Ile Ile Arg Cys Leu Ser Ser Ser Ala Val Ala Asn  
 290 295 300  
 Arg Ser Lys Lys Ser Arg Ala Leu Phe Leu Ser Ala Ala Val Phe Cys  
 305 310 315 320  
 Ile Phe Ile Ile Cys Phe Gly Pro Thr Asn Val Leu Leu Ile Ala His  
 325 330 335  
 Tyr Ser Phe Leu Ser His Thr Ser Thr Thr Glu Ala Ala Tyr Phe Ala  
 340 345 350  
 Tyr Leu Leu Cys Val Cys Val Ser Ser Ile Ser Ser Cys Ile Asp Pro  
 355 360 365  
 Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser  
 370 375 380  
 Ile Leu Cys Cys Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser  
 385 390 395 400

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Gly Gln Leu Met Ala Ser Lys Met Asp Thr Cys Ser Ser Asn Leu Asn  
405 410 415

Asn Ser Ile Tyr Lys Lys Leu Leu Thr  
420 425

<210> 81  
<211> 348  
<212> PRT  
<213> Homo sapiens

<400> 81  
Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Ala  
1 5 10 15

Thr Gly Val Val Arg Ser Pro Phe Glu Tyr Pro Gln Tyr Tyr Leu Ala  
20 25 30

Glu Pro Trp Gln Phe Ser Met Leu Ala Ala Tyr Met Phe Leu Leu Ile  
35 40 45

Val Leu Gly Phe Pro Ile Asn Phe Leu Thr Leu Tyr Val Thr Val Gln  
50 55 60

His Lys Lys Leu Arg Thr Pro Leu Asn Tyr Ile Leu Leu Asn Leu Ala  
65 70 75 80

Val Ala Asp Leu Phe Met Val Leu Gly Gly Phe Thr Ser Thr Leu Tyr  
85 90 95

Thr Ser Leu His Gly Tyr Phe Val Phe Gly Pro Thr Gly Cys Asn Leu  
100 105 110

Glu Gly Phe Phe Ala Thr Leu Gly Gly Glu Ile Ala Leu Trp Ser Leu  
115 120 125

Val Val Leu Ala Ile Glu Arg Tyr Val Val Val Cys Lys Pro Met Ser  
130 135 140

Asn Phe Arg Phe Gly Glu Asn His Ala Ile Met Gly Val Ala Phe Thr  
145 150 155 160

Trp Val Met Ala Leu Ala Cys Ala Ala Pro Pro Leu Ala Gly Trp Ser  
165 170 175

Arg Tyr Ile Pro Glu Gly Leu Gln Cys Ser Cys Gly Ile Asp Tyr Tyr  
180 185 190

Thr Leu Lys Pro Glu Val Asn Asn Glu Ser Phe Val Ile Tyr Met Phe  
195 200 205

Val Val His Phe Thr Ile Pro Met Ile Ile Ile Phe Phe Cys Tyr Gly  
210 215 220

Gln Leu Val Phe Thr Val Lys Glu Ala Ala Ala Gln Gln Gln Glu Ser  
225 230 235 240

Ala Thr Thr Gln Lys Ala Glu Lys Glu Val Thr Arg Met Val Ile Ile  
245 250 255

Met Val Ile Ala Phe Leu Ile Cys Trp Val Pro Tyr Ala Ser Val Ala  
 260 265 270

Phe Tyr Ile Phe Thr His Gln Gly Ser Asn Phe Gly Pro Ile Phe Met  
 275 280 285

Thr Ile Pro Ala Phe Phe Ala Lys Ser Ala Ala Ile Tyr Asn Pro Val  
 290 295 300

Ile Tyr Ile Met Met Asn Lys Gln Phe Arg Asn Cys Met Leu Thr Thr  
 305 310 315 320

Ile Cys Cys Gly Lys Asn Pro Leu Gly Asp Asp Glu Ala Ser Ala Thr  
 325 330 335

Val Ser Lys Thr Glu Thr Ser Gln Val Ala Pro Ala  
 340 345

<210> 82

<211> 460

<212> PRT

<213> Rattus Norvegicus

<400> 82

Met Asn Thr Ser Val Pro Pro Ala Val Ser Pro Asn Ile Thr Val Leu  
 1 5 10 15

Ala Pro Gly Lys Gly Pro Trp Gln Val Ala Phe Ile Gly Ile Thr Thr  
 20 25 30

Gly Leu Leu Ser Leu Ala Thr Val Thr Gly Asn Leu Leu Val Leu Ile  
 35 40 45

Ser Phe Lys Val Asn Thr Glu Leu Lys Thr Val Asn Asn Tyr Phe Leu  
 50 55 60

Leu Ser Leu Ala Cys Ala Asp Leu Ile Ile Gly Thr Phe Ser Met Asn  
 65 70 75 80

Leu Tyr Thr Thr Tyr Leu Leu Met Gly His Trp Ala Leu Gly Thr Leu  
 85 90 95

Ala Cys Asp Leu Trp Leu Ala Leu Asp Tyr Val Ala Ser Asn Ala Ser  
 100 105 110

Val Met Asn Leu Leu Leu Ile Ser Phe Asp Arg Tyr Phe Ser Val Thr  
 115 120 125

Arg Pro Leu Ser Tyr Arg Ala Lys Arg Thr Pro Arg Arg Ala Ala Leu  
 130 135 140

Met Ile Gly Leu Ala Trp Leu Val Ser Phe Val Leu Trp Ala Pro Ala  
 145 150 155 160

Ile Leu Phe Trp Gln Tyr Leu Val Gly Glu Arg Thr Val Leu Ala Gly  
 165 170 175

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Gln Cys Tyr Ile Gln Phe Leu Ser Gln Pro Ile Ile Thr Phe Gly Thr  
 180 185 190  
 Ala Met Ala Ala Phe Tyr Leu Pro Val Thr Val Met Cys Thr Leu Tyr  
 195 200 205  
 Trp Arg Ile Tyr Arg Glu Thr Glu Asn Arg Ala Arg Glu Leu Ala Ala  
 210 215 220  
 Leu Gln Gly Ser Glu Thr Pro Gly Lys Gly Gly Ser Ser Ser Ser  
 225 230 235 240  
 Ser Glu Arg Ser Gln Pro Gly Ala Glu Gly Ser Pro Glu Ser Pro Pro  
 245 250 255  
 Gly Arg Cys Cys Arg Cys Cys Arg Ala Pro Arg Leu Leu Gln Ala Tyr  
 260 265 270  
 Ser Trp Lys Glu Glu Glu Glu Asp Glu Gly Ser Met Glu Ser Leu  
 275 280 285  
 Thr Ser Ser Glu Gly Glu Glu Pro Gly Ser Glu Val Val Ile Lys Met  
 290 295 300  
 Pro Met Val Asp Ser Glu Ala Gln Ala Pro Thr Lys Gln Pro Pro Lys  
 305 310 315 320  
 Ser Ser Pro Asn Thr Val Lys Arg Pro Thr Lys Lys Gly Arg Asp Arg  
 325 330 335  
 Gly Gly Lys Gly Gln Lys Pro Arg Gly Lys Glu Gln Leu Ala Lys Arg  
 340 345 350  
 Lys Thr Phe Ser Leu Val Lys Glu Lys Lys Ala Ala Arg Thr Leu Ser  
 355 360 365  
 Ala Ile Leu Leu Ala Phe Ile Leu Thr Trp Thr Pro Tyr Asn Ile Met  
 370 375 380  
 Val Leu Val Ser Thr Phe Cys Lys Asp Cys Val Pro Glu Thr Leu Trp  
 385 390 395 400  
 Glu Leu Gly Tyr Trp Leu Cys Tyr Val Asn Ser Thr Val Asn Pro Met  
 405 410 415  
 Cys Tyr Ala Leu Cys Asn Lys Ala Phe Arg Asp Thr Phe Arg Leu Leu  
 420 425 430  
 Leu Leu Cys Arg Trp Asp Lys Arg Arg Trp Arg Lys Ile Pro Lys Arg  
 435 440 445  
 Pro Gly Ser Val His Arg Thr Pro Ser Arg Gln Cys  
 450 455 460

<210> 83  
<211> 350  
<212> PRT  
<213> *Homo sapiens*

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<400> 83  
 Met Ser Asn Ile Thr Asp Pro Gln Met Trp Asp Phe Asp Asp Leu Asn  
 1 5 10 15

Phe Thr Gly Met Pro Pro Ala Asp Glu Asp Tyr Ser Pro Cys Met Leu  
 20 25 30

Glu Thr Glu Thr Leu Asn Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu  
 35 40 45

Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met Leu Val Ile  
 50 55 60

Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr Leu Leu Asn  
 65 70 75 80

Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro Ile Trp Ala  
 85 90 95

Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu Cys Lys Val  
 100 105 110

Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu Leu Leu  
 115 120 125

Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His Ala Thr Arg  
 130 135 140

Thr Leu Thr Gln Lys Arg His Leu Val Lys Phe Val Cys Leu Gly Cys  
 145 150 155 160

Trp Gly Leu Ser Met Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg Gln  
 165 170 175

Ala Tyr His Pro Asn Asn Ser Ser Pro Val Cys Tyr Glu Val Leu Gly  
 180 185 190

Asn Asp Thr Ala Lys Trp Arg Met Val Leu Arg Ile Leu Pro His Thr  
 195 200 205

Phe Gly Phe Ile Val Pro Leu Phe Val Met Leu Phe Cys Tyr Gly Phe  
 210 215 220

Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys His Arg Ala  
 225 230 235 240

Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp Leu  
 245 250 255

Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr Gln Val  
 260 265 270

Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg Ala Leu Asp  
 275 280 285

Ala Thr Glu Ile Leu Gly Phe Leu His Ser Cys Leu Asn Pro Ile Ile  
 290 295 300

Tyr Ala Phe Ile Gly Gln Asn Phe Arg His Gly Phe Leu Lys Ile Leu  
 305 310 315 320

Ala Met His Gly Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val  
325 330 335

Thr	Ser	Tyr	Thr	Ser	Ser	Ser	Val	Asn	Val	Ser	Ser	Asn	Leu
			340					345					350

<210> 84  
<211> 601  
<212> PRT  
<213> Drosophila melanogaster

<400> 84  
Met Pro Ser Ala Asp Gln Ile Leu Phe Val Asn Val Thr Thr Thr Val  
1 5 10 15

Ala Ala Ala Ala Leu Thr Ala Ala Ala Ala Val Ser Thr Thr Lys Ser  
20 25 30

Gly Asn Gly Asn Ala Ala Arg Gly Tyr Thr Asp Ser Asp Asp Asp Ala  
35 40 45

Gly Met Gly Thr Glu Ala Val Ala Asn Ile Ser Gly Ser Leu Val Glu  
       50                 55                 60

Gly	Leu	Thr	Thr	Val	Thr	Ala	Ala	Leu	Ser	Thr	Ala	Gln	Ala	Asp	Lys
65					70					75					80

Asp Ser Ala Gly Glu Cys Glu Gly Ala Val Glu Glu Leu His Ala Ser  
85 90 95

Ile Leu Gly Leu Gln Leu Ala Val Pro Glu Trp Glu Ala Leu Leu Thr  
100 105 110

Ala Leu Val Leu Ser Val Ile Ile Val Leu Thr Ile Ile Gly Asn Ile  
115 120 125

Leu Val Ile Leu Ser Val Phe Thr Tyr Lys Pro Leu Arg Ile Val Gln  
130 135 140

Asn Phe Phe Ile Val Ser Leu Ala Val Ala Asp Leu Thr Val Ala Leu  
145 150 155 160

Leu Val Leu Pro Phe Asn Val Ala Tyr Ser Ile Leu Gly Arg Trp Glu  
165 170 175

Phe Gly Ile His Leu Cys Lys Leu Trp Leu Thr Cys Asp Val Ile Cys  
180 185 190

Cys Thr Ser Ser Ile Leu Asn Leu Cys Ala Ile Ala Leu Asp Arg Tyr  
195 200 205

Trp Ala Ile Thr Asp Pro Ile Asn Tyr Ala Gln Lys Arg Thr Val Gly  
210 215 220

Arg Val Leu Leu Leu Ile Ser Gly Val Trp Leu Leu Ser Leu Leu Ile  
225 230 235 240

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Ser Ser Pro Pro Leu Ile Gly Trp Asn Asp Trp Pro Asp Glu Phe Thr  
 245 250 255  
 Ser Ala Thr Pro Cys Glu Leu Thr Ser Gln Arg Gly Tyr Val Ile Tyr  
 260 265 270  
 Ser Ser Leu Gly Ser Phe Phe Ile Pro Leu Ala Ile Met Thr Ile Val  
 275 280 285  
 Tyr Ile Glu Ile Phe Val Ala Thr Arg Arg Arg Leu Arg Glu Arg Ala  
 290 295 300  
 Arg Ala Asn Lys Leu Asn Thr Ile Ala Leu Lys Ser Thr Glu Leu Glu  
 305 310 315 320  
 Pro Met Ala Asn Ser Ser Pro Val Ala Ala Ser Asn Ser Gly Ser Lys  
 325 330 335  
 Ser Arg Leu Leu Ala Ser Trp Leu Cys Cys Gly Arg Asp Arg Ala Gln  
 340 345 350  
 Phe Ala Thr Pro Met Ile Gln Asn Asp Gln Glu Ser Ile Ser Ser Glu  
 355 360 365  
 Thr His Gln Pro Gln Asp Ser Ser Lys Ala Gly Pro His Gly Asn Ser  
 370 375 380  
 Asp Pro Gln Gln Gln His Val Val Val Leu Val Lys Lys Ser Arg Arg  
 385 390 395 400  
 Ala Lys Thr Lys Asp Ser Ile Lys His Gly Lys Thr Arg Gly Gly Arg  
 405 410 415  
 Lys Ser Gln Ser Ser Ser Thr Cys Glu Pro His Gly Glu Gln Gln Leu  
 420 425 430  
 Leu Pro Ala Gly Gly Asp Gly Gly Ser Cys Gln Pro Gly Gly His  
 435 440 445  
 Ser Gly Gly Gly Lys Ser Asp Ala Glu Ile Ser Thr Glu Ser Gly Ser  
 450 455 460  
 Asp Pro Lys Gly Cys Ile Gln Val Cys Val Thr Gln Ala Asp Glu Gln  
 465 470 475 480  
 Thr Ser Leu Lys Leu Thr Pro Pro Gln Ser Ser Thr Gly Val Ala Ala  
 485 490 495  
 Val Ser Val Thr Pro Leu Gln Lys Lys Thr Ser Gly Val Asn Gln Phe  
 500 505 510  
 Ile Glu Glu Lys Gln Lys Ile Ser Leu Ser Lys Glu Arg Arg Ala Ala  
 515 520 525  
 Arg Thr Leu Gly Ile Ile Met Gly Val Phe Val Ile Cys Trp Leu Pro  
 530 535 540  
 Phe Phe Leu Met Tyr Val Ile Leu Pro Phe Cys Gln Thr Cys Cys Pro  
 545 550 555 560

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Thr Asn Lys Phe Lys Asn Phe Ile Thr Trp Leu Gly Tyr Ile Asn Ser  
565 570 575

Gly Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Leu Asp Tyr Arg Arg  
580 585 590

Ala Phe Lys Arg Leu Leu Gly Leu Asn  
595 600

<210> 85

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 85

agatgccacc ttccaggct

19

<210> 86

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 86

ggagaagtgc atggccctc

19

<210> 87

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 87

tctcatcgtc tgactcctcg tcgttgg

27

<210> 88

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 88

ggcggtgcac acagttat

18

<210> 89  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 89 21  
agagagcgct ccaaatacca t

<210> 90  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 90  
Lys Arg Arg Ser  
1

<210> 91  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 91  
Ser Ser Ile Asp  
1

<210> 92  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 92  
Ser Arg Gln Asp  
1

<210> 93  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 93  
Gly Ser Ala Val Gly Trp  
1 5

<210> 94  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 94  
Gly Leu Gly Phe Gly Val  
1 5

<210> 95

<211> 6

<212> PRT

<213> Homo sapiens

<400> 95

Gly Gly Ser Val Ala Met  
1 5

<210> 96

<211> 6

<212> PRT

<213> Homo sapiens

<400> 96

Gly Val Ile Cys Thr Ala  
1 5

<210> 97

<211> 6

<212> PRT

<213> Homo sapiens

<400> 97

Gly Ser Glu Pro Ala Lys  
1 5

<210> 98

<211> 6

<212> PRT

<213> Homo sapiens

<400> 98

Gly Leu Val Thr Thr Ile  
1 5

<210> 99

<211> 4

<212> PRT

<213> Homo sapiens

<400> 99

Gln Gly Lys Arg  
1

<210> 100

<211> 4

<212> PRT

<213> Homo sapiens

<400> 100

Lys Arg Arg Ser  
1

<210> 101  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 101  
Arg Arg Phe Ser  
1

<210> 102  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 102  
Arg Arg Ala Ser  
1

<210> 103  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 103  
Arg Arg Arg Ser  
1

<210> 104  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 104  
Ser Ser Ile Asp  
1

<210> 105  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 105  
Ser Ser Asp Glu  
1

<210> 106  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 106  
Thr Ser Leu Glu  
1

<210> 107  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 107  
Ser Ala Leu Glu  
1

<210> 108  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 108  
Ser His Asp Asp  
1

<210> 109  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 109  
Ser Gly Glu Asp  
1

<210> 110  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 110  
Ser Ala Leu Asp  
1

<210> 111  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 111  
Thr Ala Phe Glu  
1

<210> 112  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 112  
Ser Trp Gly Glu  
1

<210> 113  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 113  
Ser Pro Ser Glu  
1

<210> 114  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 114  
Arg Ser Leu Asp Tyr Gly Tyr  
1 5

<210> 115  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 115  
Gly Ser Ala Val Gly Trp  
1 5

<210> 116  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 116  
Gly Leu Gly Phe Gly Val  
1 5

<210> 117  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 117  
Gly Gly Ser Val Ala Met  
1 5

<210> 118  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 118  
Gly Val Ile Cys Thr Ala  
1 5

<210> 119  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 119  
Gly Ser Glu Pro Ala Lys  
1 5

<210> 120  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 120  
Gly Leu Val Thr Thr Ile  
1 5

<210> 121  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 121  
Gly Ala Asp Pro Gly Glu  
1 5

<210> 122  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 122  
Gly Leu Ser Ala Ser Trp  
1 5

<210> 123  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 123  
Gly Gly Leu Arg Ala Ala  
1 5

<210> 124  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 124  
Gly Gly Gly Gly Ser Thr  
1 5

<210> 125  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 125  
Gln Gly Lys Arg  
1

<210> 126  
<211> 458  
<212> PRT  
<213> Mus Musculus

<400> 126  
Met Thr Lys Glu Met Thr Glu Asn Gln Arg Leu Cys Pro His Glu Arg  
1 5 10 15

Glu Asp Ala Asp Cys Ser Ser Glu Ser Val Lys Phe Asp Ala Arg Ser  
20 25 30

Met Thr Ala Ser Leu Pro His Ser Thr Lys Asn Gly Pro Ser Val Gln  
35 40 45

Glu Lys Leu Lys Ser Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu  
50 55 60

Val Phe Ala Val Leu Ile Pro Val Val Gly Ile Val Thr Ala Gln Leu  
65 70 75 80

Leu Asn Trp Glu Met Lys Asn Cys Leu Val Cys Ser Arg Asn Thr Ser  
85 90 95

Asp Thr Ser Gln Gly Pro Met Glu Lys Glu Asn Thr Ser Asn Val Glu  
100 105 110

Met Arg Phe Thr Ile Ile Met Ala His Met Lys Asp Met Glu Glu Arg  
115 120 125

Ile Gln Ser Ile Ser Asn Ser Lys Ala Asp Leu Ile Asp Thr Gly Arg  
130 135 140

Phe Gln Asn Phe Ser Met Ala Thr Asp Gln Arg Leu Asn Asp Ile Leu  
145 150 155 160

Leu Gln Leu Asn Ser Leu Ile Leu Ser Val Gln Glu His Gly Asn Ser  
165 170 175

Leu Asp Ala Ile Ser Lys Ser Leu Gln Ser Leu Asn Met Thr Leu Leu  
180 185 190

Asp Val Gln Leu His Thr Glu Thr Leu His Val Arg Val Arg Glu Ser  
195 200 205

Thr Ala Lys Gln Gln Glu Asp Ile Ser Lys Leu Glu Glu Arg Val Tyr  
210 215 220

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Lys Val Ser Ala Glu Val Gln Ser Val Lys Glu Glu Gln Ala His Val			
225	230	235	240
Glu Gln Glu Val Lys Gln Glu Val Arg Val Leu Asn Asn Ile Thr Asn			
245	250	255	
Asp Leu Arg Leu Lys Asp Trp Glu His Ser Gln Thr Leu Lys Asn Ile			
260	265	270	
Thr Phe Ile Gln Gly Pro Pro Gly Pro Gln Gly Glu Lys Gly Asp Arg			
275	280	285	
Gly Leu Thr Gly Gln Thr Gly Pro Pro Gly Ala Pro Gly Ile Arg Gly			
290	295	300	
Ile Pro Gly Val Lys Gly Asp Arg Gly Gln Ile Gly Phe Pro Gly Gly			
305	310	315	320
Arg Gly Asn Pro Gly Ala Pro Gly Lys Pro Gly Arg Ser Gly Ser Pro			
325	330	335	
Gly Pro Lys Gly Gln Lys Gly Glu Lys Gly Ser Val Gly Gly Ser Thr			
340	345	350	
Pro Leu Lys Thr Val Arg Leu Val Gly Gly Ser Gly Ala His Glu Gly			
355	360	365	
Arg Val Glu Ile Phe His Gln Gly Gln Trp Gly Thr Ile Cys Asp Asp			
370	375	380	
Arg Trp Asp Ile Arg Ala Gly Gln Val Val Cys Arg Ser Leu Gly Tyr			
385	390	395	400
Gln Glu Val Leu Ala Val His Lys Arg Ala His Phe Gly Gln Gly Thr			
405	410	415	
Gly Pro Ile Trp Leu Asn Glu Val Met Cys Phe Gly Arg Glu Ser Ser			
420	425	430	
Ile Glu Asn Cys Lys Ile Asn Gln Trp Gly Val Leu Ser Cys Ser His			
435	440	445	
Ser Glu Asp Ala Gly Val Thr Cys Thr Ser			
450	455		

<210> 127

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Xaa at position 2 and 4 may be any amino acid  
except Pro

<220>

<223> Xaa at position 3 may be Ser or Thr

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<220>

<223> Description of Artificial Sequence: Amidation  
consensus site

<400> 127

Asn Xaa Xaa Xaa  
1

<210> 128

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence

<220>

<223> Xaa at position 2 can be between 4 and 14 amino  
acids

<220>

<223> Xaa at position, if present, may be between 0 or 2  
amino acids

<220>

<223> Xaa at position 6 may be between 2 and 4 amino  
acids

<220>

<223> Xaa at position 8 may be between 6 and 12 amino  
acids

<220>

<223> Xaa at position 10 may be between 6 and 10 amino  
acids

<400> 128

Cys Xaa Cys Xaa Cys Xaa Cys Xaa Cys Xaa Cys  
1 5 10

<210> 129

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence

<220>

<223> Xaa at position 2 may be 4 or 6 amino acids

<220>

<223> Xaa at position 6 may be 5 or 10 amino acids

<220>

<223> Xaa at position 8 may be 0 or 2 amino acids

&lt;220&gt;

&lt;223&gt; Xaa at position 10 may be 7 or 11 amino acids

&lt;220&gt;

&lt;223&gt; Xaa at position 12 may be 4 or 6 amino acids

&lt;400&gt; 129

Cys	Xaa	Phe	Tyr	His	Xaa	Cys	Xaa	Cys	Xaa	Cys	Xaa	Asp	Asn	Glu	Gln
1				5				10						15	

Ser	Lys	Pro	Xaa	Xaa	Cys
			20		

&lt;210&gt; 130

&lt;211&gt; 39

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 130

Cys	Arg	Gln	Gln	Glu	Phe	Lys	Asp	Arg	Ser	Gly	Asn	Cys	Val	Leu	Cys
1				5				10					15		

Lys	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	Gly
				20				25				30			

Tyr	Gly	Glu	Asp	Ala	Gln	Cys
		35				

&lt;210&gt; 131

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 131

Cys	Arg	Pro	His	Arg	Phe	Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys
1				5					10			15			

Pro	Cys	Ala	Asp	Cys	Ala	Leu	Val	Asn	Arg	Phe	Gln	Arg	Ala	Asn	Cys
				20				25			30				

Ser	His	Thr	Ser	Asp	Ala	Val	Cys
			35			40	

&lt;210&gt; 132

&lt;211&gt; 39

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 132

Cys	Arg	Gln	Gln	Glu	Phe	Lys	Asp	Arg	Ser	Gly	Asn	Cys	Val	Leu	Cys
1				5				10					15		

Lys	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	Gly
				20				25			30				

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Tyr Gly Glu Asp Ala Gln Cys  
35

<210> 133  
<211> 40  
<212> PRT  
<213> Mus musculus

<400> 133  
Cys Arg Pro His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys  
1 5 10 15

Pro Cys Ala Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys  
20 25 30

Ser His Thr Ser Asp Ala Val Cys  
35 40

<210> 134  
<211> 29  
<212> PRT  
<213> Mus musculus

<400> 134  
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala  
1 5 10 15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys  
20 25

<210> 135  
<211> 29  
<212> PRT  
<213> Mus musculus

<400> 135  
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala  
1 5 10 15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys  
20 25

<210> 136  
<211> 25  
<212> PRT  
<213> Mus musculus

<400> 136  
Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala Thr Val Leu Leu Ala  
1 5 10 15

Leu Leu Ile Leu Cys Val Ile Tyr Cys  
20 25

<210> 137  
<211> 31  
<212> PRT  
<213> Homo sapiens

<400> 137  
Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val Phe Val Val Ser Leu  
1 5 10 15  
  
Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile Leu Lys Met Lys  
20 25 30

<210> 138  
<211> 31  
<212> PRT  
<213> Homo sapiens

<400> 138  
Phe Ser Met Leu Ala Ala Tyr Met Phe Leu Leu Ile Val Leu Gly Phe  
1 5 10 15  
  
Pro Ile Asn Phe Leu Thr Leu Tyr Val Thr Val Gln His Lys Lys  
20 25 30

<210> 139  
<211> 31  
<212> PRT  
<213> Rattus Norvegicus

<400> 139  
Val Ala Phe Ile Gly Ile Thr Thr Gly Leu Leu Ser Leu Ala Thr Val  
1 5 10 15  
  
Thr Gly Asn Leu Leu Val Leu Ile Ser Phe Lys Val Asn Thr Glu  
20 25 30

<210> 140  
<211> 31  
<212> PRT  
<213> Homo sapiens

<400> 140  
Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu Val Phe Leu Leu Ser Leu  
1 5 10 15  
  
Leu Gly Asn Ser Leu Val Met Leu Val Ile Leu Tyr Ser Arg Val  
20 25 30

<210> 141  
<211> 31  
<212> PRT  
<213> Drosophila melanogaster

<400> 141  
Ala Leu Leu Thr Ala Leu Val Leu Ser Val Ile Ile Val Leu Thr Ile  
1 5 10 15

Ile Gly Asn Ile Leu Val Ile Leu Ser Val Phe Thr Tyr Lys Pro  
20 25 30

<210> 142  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 142  
Val Val Tyr Met Leu His Leu Ala Thr Ala Asp Val Leu Phe Val Ser  
1 5 10 15

Val Leu Pro Phe Lys Ile Ser Tyr Tyr Phe Ser Gly  
20 25

<210> 143  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 143  
Asn Tyr Ile Leu Leu Asn Leu Ala Val Ala Asp Leu Phe Met Val Leu  
1 5 10 15

Gly Gly Phe Thr Ser Thr Leu Tyr Thr Ser Leu His  
20 25

<210> 144  
<211> 28  
<212> PRT  
<213> Rattus Norvegicus

<400> 144  
Asn Tyr Phe Leu Leu Ser Leu Ala Cys Ala Asp Leu Ile Ile Gly Thr  
1 5 10 15

Phe Ser Met Asn Leu Tyr Thr Tyr Leu Leu Met  
20 25

<210> 145  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 145  
Asp Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu  
1 5 10 15

Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly  
20 25

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<210> 146  
<211> 28  
<212> PRT  
<213> Drosophila melanogaster

<400> 146  
Asn Phe Phe Ile Val Ser Leu Ala Val Ala Asp Leu Thr Val Ala Leu  
1 5 10 15  
  
Leu Val Leu Pro Phe Asn Val Ala Tyr Ser Ile Leu  
20 25

<210> 147  
<211> 25  
<212> PRT  
<213> Homo sapiens

<400> 147  
Arg Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu  
1 5 10 15  
  
Leu Met Thr Val Ile Ser Ile Asp Arg  
20 25

<210> 148  
<211> 25  
<212> PRT  
<213> Homo sapiens

<400> 148  
Asn Leu Glu Gly Phe Phe Ala Thr Leu Gly Gly Glu Ile Ala Leu Trp  
1 5 10 15  
  
Ser Leu Val Val Leu Ala Ile Glu Arg  
20 25

<210> 149  
<211> 25  
<212> PRT  
<213> Rattus Norvegicus

<400> 149  
Asp Leu Trp Leu Ala Leu Asp Tyr Val Ala Ser Asn Ala Ser Val Met  
1 5 10 15  
  
Asn Leu Leu Leu Ile Ser Phe Asp Arg  
20 25

<210> 150  
<211> 25  
<212> PRT  
<213> Homo sapiens

<400> 150  
Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu  
1 5 10 15

Leu Leu Ala Cys Ile Ser Val Asp Arg  
20 25

<210> 151  
<211> 25  
<212> PRT  
<213> Drosophila melanogaster

<400> 151  
Lys Leu Trp Leu Thr Cys Asp Val Leu Cys Cys Thr Ser Ser Ile Leu  
1 5 10 15

Asn Leu Cys Ala Ile Ala Leu Asp Arg  
20 25

<210> 152  
<211> 27  
<212> PRT  
<213> Homo sapiens

<400> 152  
Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu Ala Ile Trp Ala Leu Ala  
1 5 10 15

Ile Ala Gly Val Val Pro Leu Val Leu Lys Glu  
20 25

<210> 153  
<211> 27  
<212> PRT  
<213> Homo sapiens

<400> 153  
Gly Glu Asn His Ala Ile Met Gly Val Ala Phe Thr Trp Val Met Ala  
1 5 10 15

Leu Ala Cys Ala Ala Pro Pro Leu Ala Gly Trp  
20 25

<210> 154  
<211> 27  
<212> PRT  
<213> Rattus Norvegicus

<400> 154  
Thr Pro Arg Arg Ala Ala Leu Met Ile Gly Leu Ala Trp Leu Val Ser  
1 5 10 15  
  
Phe Val Leu Trp Ala Pro Ala Ile Leu Phe Trp  
20 25

- 130 -

<210> 155  
<211> 27  
<212> PRT  
<213> Homo sapiens

<400> 155  
Lys Arg His Leu Val Lys Phe Val Cys Leu Gly Cys Trp Gly Leu Ser  
1 5 10 15

Met Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg  
20 25

<210> 156  
<211> 27  
<212> PRT  
<213> Drosophila melanogaster

<400> 156  
Thr Val Gly Arg Val Leu Leu Leu Ile Ser Gly Val Trp Leu Leu Ser  
1 5 10 15

Leu Leu Ile Ser Ser Pro Pro Leu Ile Gly Trp  
20 25

<210> 157  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 157  
Ala Tyr Tyr Phe Ser Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu  
1 5 10 15

Ile Ile Ser Thr Val Cys Tyr Val Ser Ile Ile Arg Cys  
20 25

<210> 158  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 158  
Glu Ser Phe Val Ile Tyr Met Phe Val Val His Phe Thr Ile Pro Met  
1 5 10 15

Ile Ile Ile Phe Phe Cys Tyr Gly Gln Leu Val Phe Thr  
20 25

<210> 159  
<211> 29  
<212> PRT  
<213> Rattus Norvegicus

<400> 159  
Pro Ile Ile Thr Phe Gly Thr Ala Met Ala Ala Phe Tyr Leu Pro Val  
1 5 10 15

- 131 -

Thr Val Met Cys Thr Leu Tyr Trp Arg Ile Tyr Arg Glu  
20 25

<210> 160  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 160  
Met Val Leu Arg Ile Leu Pro His Thr Phe Gly Phe Ile Val Pro Leu  
1 5 10 15

Phe Val Met Leu Phe Cys Tyr Gly Phe Thr Leu Arg Thr  
20 25

<210> 161  
<211> 29  
<212> PRT  
<213> Drosophila melanogaster

<400> 161  
Arg Gly Tyr Val Ile Tyr Ser Ser Leu Gly Ser Phe Phe Ile Pro Leu  
1 5 10 15

Ala Ile Met Thr Ile Val Tyr Ile Glu Ile Phe Val Ala  
20 25

<210> 162  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 162  
Phe Leu Ser Ala Ala Val Phe Cys Ile Phe Ile Ile Cys Phe Gly Pro  
1 5 10 15

Thr Asn Val Leu Leu Ile Ala His Tyr Ser Phe Leu  
20 25

<210> 163  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 163  
Arg Met Val Ile Ile Met Val Ile Ala Phe Leu Ile Cys Trp Val Pro  
1 5 10 15

Tyr Ala Ser Val Ala Phe Tyr Ile Phe Thr His Gln  
20 25

<210> 164  
<211> 28  
<212> PRT  
<213> Rattus Norvegicus

<400> 164  
Arg Thr Leu Ser Ala Ile Leu Leu Ala Phe Ile Leu Thr Trp Thr Pro  
1 5 10 15  
  
Tyr Asn Ile Met Val Leu Val Ser Thr Phe Cys Lys  
20 25

<210> 165  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 165  
Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp Leu Pro  
1 5 10 15  
  
Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg  
20 25

<210> 166  
<211> 28  
<212> PRT  
<213> Drosophila melanogaster

<400> 166  
Arg Thr Leu Gly Ile Ile Met Gly Val Phe Val Ile Cys Trp Leu Pro  
1 5 10 15  
  
Phe Phe Leu Met Tyr Val Ile Leu Pro Phe Cys Gln  
20 25

<210> 167  
<211> 33  
<212> PRT  
<213> Homo sapiens

<400> 167  
Glu Ala Ala Tyr Phe Ala Tyr Leu Leu Cys Val Cys Val Ser Ser Ile  
1 5 10 15  
  
Ser Ser Cys Ile Asp Pro Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys  
20 25 30  
  
Gln

<210> 168  
<211> 33  
<212> PRT  
<213> Homo sapiens

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<400> 168

Asn Phe Gly Pro Ile Phe Met Thr Ile Pro Ala Phe Phe Ala Lys Ser  
1 5 10 15

Ala Ala Ile Tyr Asn Pro Val Ile Tyr Ile Met Met Asn Lys Gln Phe  
20 25 30

Arg

<210> 169

<211> 33

<212> PRT

<213> Rattus Norvegicus

<400> 169

Cys Val Pro Glu Thr Leu Trp Glu Leu Gly Tyr Trp Leu Cys Tyr Val  
1 5 10 15

Asn Ser Thr Val Asn Pro Met Cys Tyr Ala Leu Cys Asn Lys Ala Phe  
20 25 30

Arg

<210> 170

<211> 33

<212> PRT

<213> Homo sapiens

<400> 170

Asn Asn Ile Gly Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Phe Leu  
1 5 10 15

His Ser Cys Leu Asn Pro Ile Ile Tyr Ala Phe Ile Gly Gln Asn Phe  
20 25 30

Arg

<210> 171

<211> 33

<212> PRT

<213> Drosophila melanogaster

<400> 171

Cys Pro Thr Asn Lys Phe Lys Asn Phe Ile Thr Trp Leu Gly Tyr Ile  
1 5 10 15

Asn Ser Gly Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Leu Asp Tyr  
20 25 30

Arg

<210> 172  
<211> 174  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: 7  
transmembrane receptor consensus sequence

<400> 172  
Gly Asn Ile Leu Val Ile Trp Val Ile Cys Arg Tyr Arg Arg Met Arg  
1 5 10 15

Thr Pro Met Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu  
20 25 30

Phe Ser Leu Phe Thr Met Pro Phe Trp Met Val Tyr Tyr Val Met Gln  
35 40 45

Gly Arg Trp Pro Phe Gly Asp Phe Met Cys Arg Ile Trp Met Tyr Phe  
50 55 60

Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr Cys Ile Ser  
65 70 75 80

Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg Tyr Met Arg  
85 90 95

Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile Ile Ile Trp  
100 105 110

Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met Phe Arg Trp  
115 120 125

Ser Thr Tyr Arg Asp Glu Asn Glu Trp Asn Met Thr Trp Cys Met Ile  
130 135 140

Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile Leu Met Thr  
145 150 155 160

Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu Phe  
165 170

<210> 173  
<211> 168  
<212> PRT  
<213> Homo sapiens

<400> 173  
Ala Asn Ala Trp Gly Ile Leu Ser Val Gly Ala Lys Gln Lys Lys Trp  
1 5 10 15

Lys Pro Leu Glu Phe Leu Leu Cys Thr Leu Ala Ala Thr His Met Leu  
20 25 30

Asn Val Ala Val Pro Ile Ala Thr Tyr Ser Val Val Gln Leu Arg Arg  
35 40 45

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Gln Arg Pro Asp Phe Glu Trp Asn Glu Gly Leu Cys Lys Val Phe Val  
50 55 60

Ser Thr Phe Tyr Thr Leu Thr Leu Ala Thr Cys Phe Ser Val Thr Ser  
65 70 75 80

Leu Ser Tyr His Arg Met Trp Met Val Cys Trp Pro Val Asn Tyr Arg  
85 90 95

Leu Ser Asn Ala Lys Lys Gln Ala Val His Thr Val Met Gly Ile Trp  
100 105 110

Met Val Ser Phe Ile Leu Ser Ala Leu Pro Ala Val Gly Trp His Asp  
115 120 125

Thr Ser Glu Arg Phe Tyr Thr His Gly Cys Arg Phe Ile Val Ala Glu  
130 135 140

Ile Gly Leu Gly Phe Gly Val Cys Phe Leu Leu Leu Val Gly Gly Ser  
145 150 155 160

Val Ala Met Gly Val Ile Cys Thr  
165

<210> 174

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence

<400> 174

Ile Gln Glu Arg Met Asn Glu Leu Asn Asp Arg Trp Glu Arg Leu Lys  
1 5 10 15

Glu Leu Met Glu Gln Arg Arg Gln Met Leu Glu Asp Ser Met Arg Leu  
20 25 30

Gln Gln Phe Phe Arg Asp Met Asp Glu Glu Glu Ser Trp Ile Asn Glu  
35 40 45

Lys Glu Gln Ile Leu Asn Ser Asp Asp Tyr Gly Lys Asp Leu Thr Ser  
50 55 60

Val Gln Asn Leu Leu Lys Lys His Gln Ala Phe Glu Ala Asp Ile Ala  
65 70 75 80

Ala His Glu Asp Arg Ile Gln Ala Leu Asn Glu Phe Ala Gln Gln Leu  
85 90 95

Ile Gln Glu Asn His Tyr Ala Ser Glu Glu  
100 105

- 136 -

<210> 175  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 175  
Phe Ser Ser Leu Arg Ala Asp Ala Ser Ala Pro Trp Met Ala Leu Cys  
1 5 10 15  
  
Val Leu Trp Cys Ser Val Ala Gln Ala Leu Leu Leu Pro Val Phe Leu  
20 25 30  
  
Trp Ala Cys Asp Arg Tyr Arg Ala Asp Leu Lys Ala Val Arg Glu Lys  
35 40 45  
  
Cys Met Ala Leu Met Ala Asn Asp Glu Glu Ser Asp Asp Glu Thr Ser  
50 55 60  
  
Leu Glu Gly Gly Ile Ser Pro Asp Leu Val Leu Glu Arg Ser Leu Asp  
65 70 75 80  
  
Tyr Gly Tyr Gly Gly Asp Phe Val Ala Leu Asp Arg Met Ala Lys Tyr  
85 90 95  
  
Glu Ile Ser Ala Leu Glu Gly Leu Pro Gln  
100 105

<210> 176  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Xaa at position 2 may be any amino acid except:  
Glu, Asp, Arg, Lys, His, Phe, Pro, Tyr, or Trp  
  
<220>  
<223> Xaa at position 5 may be ser, Thr, Ala, Gly, Cys  
or Asn  
  
<220>  
<223> Xaa at position 6 may be any amino acid except Pro  
  
<220>  
<223> Description of Artificial Sequence: Amidation  
consensus site  
  
<400> 176  
Gly Xaa Xaa Xaa Xaa Xaa  
1 5